

1	11	21	31	41	51	61	71	81	91
SEQ 3	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 6	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 8	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 10	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 12	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 14	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 16	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 19	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 22	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 24	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 27	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 30	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 33	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 35	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 38	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 40	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 42	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 44	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 83	MTVQSOQOSQ	AIPVLLSSQ	TEPODANEK	VQNVAAKGVQ	YFNPEQLPAP	GLGNGPNT	-----	-----	-----
SEQ 85	-----	-----	-----	-----	-----	-----	-----	-----	-----
Bacteria	-----	-----	-----	-----	-----	-----	-----	-----	-----
T44612	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_625402	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_295913	-----	-----	-----	-----	-----	-----	-----	-----	-----
AF320254	-----	-----	-----	-----	-----	-----	-----	-----	-----
YB family	-----	-----	-----	-----	-----	-----	-----	-----	-----
Af4875	-----	-----	-----	-----	-----	-----	-----	-----	-----
Af4961	-----	-----	-----	-----	-----	-----	-----	-----	-----
Ca2460	-----	-----	-----	-----	-----	-----	-----	-----	-----
Nc4452	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY81	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY82	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY83	-----	-----	-----	-----	-----	-----	-----	-----	-----
A36990	-----	-----	-----	-----	-----	-----	-----	-----	-----
101	111	121	131	141	151	161	171	181	191
2	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 3	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 6	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 8	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 10	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 12	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 14	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 16	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 19	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 22	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 24	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 27	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 30	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 33	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 35	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 38	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 40	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 42	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 44	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 83	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 85	-----	-----	-----	-----	-----	-----	-----	-----	-----
Bacteria	-----	-----	-----	-----	-----	-----	-----	-----	-----
T44612	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_625402	-----	-----	-----	-----	-----	-----	-----	-----	-----
NP_295913	-----	-----	-----	-----	-----	-----	-----	-----	-----
AF320254	-----	-----	-----	-----	-----	-----	-----	-----	-----
YB family	-----	-----	-----	-----	-----	-----	-----	-----	-----
Af4875	-----	-----	-----	-----	-----	-----	-----	-----	-----
Af4961	-----	-----	-----	-----	-----	-----	-----	-----	-----
Ca2460	-----	-----	-----	-----	-----	-----	-----	-----	-----
Nc4452	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY81	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY82	-----	-----	-----	-----	-----	-----	-----	-----	-----
ScOY83	-----	-----	-----	-----	-----	-----	-----	-----	-----
A36990	-----	-----	-----	-----	-----	-----	-----	-----	-----

	201	211	221	231	241	251	261	271	281	291
SEQ 3	LAHAGRKATT VAPW-----	ISPS A1ATEKVGPGD-----	P-----							
SEQ 6	IAHAGRKAST VAPW-----	LSAN DTASEKMGW PGKVKGPTNV-----	P-----							
SEQ 8	LAHAGRKASA VAPW-----	LAAGQKSS LKADESVGGW PADVVGPSGG-----	E-----							
SEQ 10	IAHAGRKASA IAPW-----	LMNKG IVATEKVGW PDREVGPSTV-----	P-----							
SEQ 12	LGHGGRKASC QPLF-----	LHLE QVADKSVNPG ADKAVAPSAL A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
SEQ 14	LNHAGRKIVG VPFP-----	--QIQTHGW QEHCVGPTSE P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----
SEQ 16	LAHAGRKAST KAPW-----	--HYQRGKS ELAGPQEKGW PENVWAPS A-----	S-----							
SEQ 19	INHGPGRQSPF GAGT-----	--RGLW E-KVAVAPSPV P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----
SEQ 22	LAHAGRKAST PAPWHDSPFT SGEYKPREGL QVQGPPEYGGW PDDVVGPSA-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----
SEQ 24	LAHAGRKAST TAPY-----	--RG-Y TVATEQAGW ENDVVGPTN E-----	E-----	E-----	E-----	E-----	E-----	E-----	E-----	E-----
SEQ 27	LAHAGRKAST LAPW-----	--ITEARGK ALAOESENGW PDDVVGPSA-----	P-----							
SEQ 30	LSHAGRKASC VSPW-----	--LSVN AVAAEEVGGW PDNIVAPS A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
SEQ 33		--QNGVNPV KA-----	KA-----	KA-----	KA-----	KA-----	KA-----	KA-----	KA-----	KA-----
SEQ 35	IGHAGRKAST VVPW-----	--LDRK NTAP?-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 38	LSHAGRKASC VSPW-----	--LSIN AVAAKEVGGW PDNIVAPS A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
SEQ 40	LAHAGRKAST VAPW-----	--LSGG DVAGEDVNGW PDNIVAPS A-----	P-----							
SEQ 42		--LPS ERKAGEGGW PEDVVGPSG EDFTWDERS-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 44	VGHPGRQARG SVQ-----	--OHPISASD VOLKQEM-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 83	IGHAGRKASC VAPW-----	--LDAG LAAEKAAGW PDDVVGPSNE P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----
SEQ 85	LAHAGRKASD WSPP-----	--YRGEKKQ KPVIQEEDGW PDNIVAPS A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
Bacteria		--YAGQHVT P-----	RA-----							
T44612	IAHAGRKASA NRWP-----	--EGDD HIGADARGW -ETIAPS A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
NP_625402	LAHAGRKAST AOPW-----	--RGG APVGADAYWQ -QPLAPS A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----	A-----
NP_295913	LAHAGRKAST YAPW-----	--RGK GAVPAELGGW -QVIGPDEN S-----	S-----	S-----	S-----	S-----	S-----	S-----	S-----	S-----
AF320254	LAHAGRKGAT KLAW-----	--EG IDEPLEAGW -ELISASPL P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----	P-----
OYE family		--YLPHSQV P-----	RA-----							
Af4875	LWATGRADP DVLA-----	--DMK -D LISS-AVPV EKGP-----	P-----							
Af4961	LWAGHRATIP QMTG-----	--SPAVSAS ATVWDSPTBC YSHPP-----	P-----							
Ca2460	LWYLGVRVANP KDLK-----	--DAGLPL IGPSP -VW DEESE-----	-----	-----	-----	-----	-----	-----	-----	-----
Nc4452	LWSLGRVANP EVLA-----	--KEGGKL LKSSS-AVPM EEGAP-----	P-----							
ScOYE1	LWLVGWAAPP DNLA-----	--RDG-LR YDSASDNVFM DABQE-----	P-----							
ScOYE2	LWLVGWAAPP DTLA-----	--RDG-LR YDSASDNVFM NAQOE-----	P-----							
ScOYE3	LWSLGRVANP DVLA-----	--RDG-LR YDCASDRVFM NATLO-----	P-----							
A36990	LWYLGVRVANA KDLK-----	--DSG-LP LIAPS-AVYVW DENSE-----	P-----							
	301	311	321	331	341	351	361	371	381	391
	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 3	TKRAIAA-GA DFWIIHNAHG YLSSSPFLSP-----	--AANNRRTDGY G-GSPENRIR LSLIEIAQLTR DAVGHPV-----	P-----							
SEQ 6	VIGRAVKA-GA DPFIIRHNAHG YLILQFPLSP-----	--AVNTRRTDGY G-GSPENRIR LSLIEIAKLTR EDVPKDMP-----	P-----							
SEQ 8	ARLAOVA-GV DVIEIIHCAHG YLILNRPFLSP-----	--VTNKRRTDAY G-GSPENRIR LSLIEIAAAIR AV1PEGM-----	P-----							
SEQ 10	CKRAIAA-GA DPFIIRHNAHG YLILNRPFLSP-----	--SSNTRRTDGY G-GSPENRIR LSLIEIAQVTR DAVGPNV-----	P-----							
SEQ 12	ARRAVEISGF DAVEIIHCAHG YLILNPEYSP-----	--ISNKRRTDGY G-GSPENRIR LFLKEVIDSVK SSIPLNDV-----	P-----							
SEQ 14	AWRAVBIKSF DAIIEIIHCAHG CLJHOPFLSK-----	--LTNKRRTDGY G-GSPENRIR FLQIENIISK RXKLET-----P-----	P-----							
SEQ 16	AORALKA-GF DLIRIHAHG YLILSEFPLSP-----	--ISNQRTDGY G-GSPENRIR VLREIISAVK SWIPEDMP-----	P-----							
SEQ 19	ARITABA-GF NOVIEIIHAAHG YLILQFPLSK-----	--KTNRRGDEY G-GSAENRIR IVGEIIKCCR RQTEAVGEE BAKKFFVVGIK LNSA-DWQA-----	P-----							
SEQ 22	AKRAIEA-GV DVIEIIHCAHG YLILTEPFLSP-----	--LSNKRRTDKY G-GSPENRIR VLIDIIXKAVR AVIPEEM-----	P-----							
SEQ 24	AKRAIEA-GF DVIEIIHCAHG YLISSTVSPA-----	--FTTNDRNDKTY G-GTPFEKRL FPMEVVHSV RKAIDPMS-----	P-----							
SEQ 27	AKRSRRA-GF DVIEIIHAA-----	--LTMRTDGY G-GSLENRIR FLLNVARRIR QEPNKG-----	P-----							
SEQ 30	AKRAIHA-GF DVIEIIHAAHG YLILQFPLSP-----	--VSNQRTDGY G-GSPENRIR VVLEIILDLIR AAIPETTP-----	P-----							
SEQ 33		--TDEY G-GSPENRIR VVLEIILDLIR AAIPETTP-----	P-----							
SEQ 35		--VFLR VSAT-DWPEP DSOFKDEPPE-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 38	KRA-RA-GF DVIEIIHAAHG YLILQFPLSP-----	--VSNQRTDGY G-GSPENRIR VVLEIIL-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 40	VIGRAVKA-GF DVIEIIHNAHG YLILHEFPLC-----	--RATPGPTST G-GSPENRIR LTMESSRRCPC QH-----	P-----							
SEQ 42	AKRAVKA-GV DVIEIIHCAHG YLILHEFPLSP-----	--ITNRTRTDGY G-GSPENRIR LLEIIVTAIVR AAAMPSSM-----	P-----							
SEQ 44	AEYLEKA-GF DGEIILHCAHG YLILQFPLSE-----	--TNTNRRTDGY G-GSLENRIR LLEIIVTAEV RPTSKNP-----	P-----							
SEQ 83	VRAVEA-GF DTIDPHPAHG YLVSSFLSP-----	--ATNKRTDKY G-GSPENRIR LALEIVEAAR AVMPEDMP-----	P-----							
SEQ 85	ARNAFEA-GY DVELHSAG YLMHGSFPLSP-----	--LTNRTDGY G-GSLENRIR FLLNVARRIR QEPNKG-----	P-----							
Bacteria		--LMVR VSAT-DWAD-----	-----	-----	-----	-----	-----	-----	-----	-----
T44612	ARRARDA-GF EMIEILHPAHG YLGQSPPFS-----	--HSNKRRTDAY G-GSPDNRIR FLLETLAIVR EW/PENLP-----	P-----							
NP_625402	ARRALNA-GF EIABEIHCAHG YLILHSEFPLSP-----	--HSNQRTDGY G-GSPENRIR PALEVA/DAIV EW/PDLP-----	P-----							
NP_295913	ARRAOVA-GF DAVEVHAAHG YLILQFPLSP-----	--LANTRTDGY G-GSPENRIR LLLEVVA/RAVR HW/PWAHL-----	P-----							
AF320254	TRMAABA-GF DILELHCAGH YLILQFPLSP-----	--LTNRTDGY G-GDLENRIR FPLLEVKAMR AMWPTNRP-----	P-----							
OYE family		--MSVR LSCH-DWFP-----	-----	-----	-----	-----	-----	-----	-----	-----
Af4875	ARNAINA-GF DGEVIIHCAHG YLILQFPLTK-----	--SCNHRDWR G-GSLENRIR PAVEVTRAVI EAVGADR-----	P-----							
Af4961	AKTAMBI-GF DGEVIIHCAHG YLILQFPLSS-----	--NWNKRRTDGY G-GSPENRIR FVLEIMDDELA ATVGEON-----	P-----							
Ca2460	AKRAIBA-GF DYIEVHSAG YLILQFPLNP-----	--ASNKRTDKY G-GSLENRIR LLLRIIDKLI GIVCAEK-----	P-----							
Nc4452	AKNAVEA-GF DGEVIIHCAHG YLILQFPLQD-----	--TCNQRTDGY G-GSLENRIR FAHVVVKAIV EAVGAEK-----	P-----							
ScOYE1	AKNSIAA-GA DGEVIIHCAHG YLILQFPLDP-----	--HSNTRRTDGY G-GSLENRIR FTLEVDALIV SAIGCHEK-----	P-----							
ScOYE2	AKNSIAA-GA DGEVIIHCAHG YLILQFPLDP-----	--HSNQRTDGY G-GSLENRIR FTLEVDAAV DAIGPEK-----	P-----							
ScOYE3	AKNSIAA-GA DGEVIIHCAHG YLILQFPLDP-----	--HSNKRRTDGY G-GTENRIR FTLEVDALI ETIGPER-----	P-----							
A36990	AKHALAE-GF DYIEVHSAG YLILQFPLNL-----	--ASNKRTDKY GCGSIENRIR LLLRVVDKLI EVVGANR-----	P-----							

	401	411	421	431	441	451	461	471	481	491
SEQ 3	-SMKSEDTVR	-FAQELVK	-Q GAVDLDIIS	GGVLAQO-	-	-K I	KSGCPAQOPPV	AVAVKKAVGD	-KLLAVAA	GMIT
SEQ 6	-SWRGVDTVR	-PAKILAA	-BT GYVLDVDS	GGTHSEQ-	-	-K I	KAGPQGQAPP	AIAVRANAVGD	-KLAVASV	GMIA
SEQ 8	-SWDM-QSSL	-ELVKLKP-	-B MGIDLVDVS	AAHIDHD-	-	-K I	NLHTTYQTDL	AGQIQRQAI-	-RAAGAST	LVGAVGLITD
SEQ 10	-SWKLSDSVD	-FAEALAA-	-Q GADIDLVDVS	GGVRAAO-	-	-K I	KSGCPAQOPPV	AVAVKKAVGD	-KLLAVATV	GT1
SEQ 12	-ATM1EDSKK-	-LADILV-	-B KGIDLVDVS	GGNDYRQPP-	-	-RSIGK	ELRPPVHPL	SKA1QHVGQ	-KLLAVCV	GGLB
SEQ 14	-ANSTEDALK-	-LADILV-	-D LGVLDVDS	GGVNAHKCS-	-	-RYLLND	DQQLSPQVSP	AKRLKSHIRSA	-RCLLAVG	GGLD
SEQ 16	-SMWDLQQT	-ELAKLKP-	-D LGVLDVDS	GGNKKDQ-	-	-K I	NVHTVYQTDL	AOQ1RAAVH8	-AGKQ1LQVG	GLVT
SEQ 19	-TDTAAEVLK-	-QIEFLPF-	-Q GQDPEVMS	GSYEDPOMAN	-GPKPERSKT	-	MARAEFFLSP	AKIIRKAVGD	-PPKLPLMTV	GGFR
SEQ 22	-SMWDLQSTO	-LAKLKP-	-D LGVLDVDS	GGNHSVAQ-	-	-K I	ELTPVYQDPL	AK1RRAVGQD	-RLLAVG	GNIN
SEQ 24	-GWE1EDTVAP	-TLAARIA-	-D GQDPEVMS	GGNHKDO-	-	-R I	EVKDCYQVPP	AEK1KDQVNG	-ILLGAV	GMIR
SEQ 27	-	-	-	-	-	-	-	-	-	-
SEQ 30	-SMWVQTC-	-QLARILP-	-K HGVDLVDVS	GGIHPKS-	-	-ATAI	KSGCPAYQVDL	AKQVKKAVGD	-SVLVSAAV	GGIK
SEQ 35	-	-	-	-	-	-	-	-	-	-
SEQ 40	-SMWVESTIK-	-ISKILIA-	-D LGVLDLVDVS	GGNHKPOO-	-	-K I	NMFNT-	-	-	-
SEQ 42	-FKP-EBAQ-	-LCAEALAAGM	-DFVTS	GTYESPG-	-	-FAHRKES	RKRKENYPIEF	ABVIRKAVKH	-MVVTTG	GPRT
SEQ 44	-TWLTIOSK-	-LAHOIA-	-D RGVDLVDVS	GGIHHMO-	-	-K V	AAAGPGYQAPL	AAKAIKKSSVG	-KMLISTV	GSIK
SEQ 83	-SMWDLQTV-	-LAKMQLB-	-ARVLDLVDVS	GGVHPVPO-	-	-K I	AVTGACOLYQ	AKAVRDALAK	-IHPDASKR	MVGA
Bacteria	-	-	-	-	-	-	-	-	-	-
T44612	-EQTLBEESI-	-ELARLRFK-	-A GGDLILSVSV	GPTIPET-	-	-NI	PWGPAPMGP1	AERVRRREAL	-PVTSAW	GFPT
NP_625402	-GWTPPDTVR	-FARLDS-	-B HGIDLVDVS	GGNPKPRV-	-	-RI	PTGPGYQVPP	AARVKAGST	-LPVAAV	GLIT
NP_295913	-GMWDLQTV-	-LSKLX-	-Y LGVLDLVDVS	GGLTAQAO-	-	-OI	EVGPGYQVPP	AAAVSRAETB	-ISVMVQ	GLIE
AF320254	-GNTADDAVA-	-IARLFLK-	-E AGAD1IDCS	GGVWRKGD-	-	-OP	VYGRMRYQTFF	ADRIIRNEVGT	-PTLAVG	AISE
OYE family	-	-	-	-	-	-	-	-	-	-
Af4875	-EL-VPQF	LIA-	-Q MN RLDLVAYLH	ANSRML-	-	-DE	EKPHDPDHN	VFVRVVMG-Q	-SS-PILLA	GGYD
Af4961	-ORV-VETWTF	-CLESCLKKAH	-NLSYV	IEPYRE-	-	-QF8YEBKD	NFLRWSMG-	LSDDVLSRFS	K1P97TPPPFS	-
Ca2460	EE---IHSY	ILOQOORAD	NGOOLAYSLV	IEPVRIG-	-	-	-	-	-	-
Nc4452	DLIP---QFED	VIRKIN-	-	-	-	-	-	-	-	-
ScOYE1	-ETGIVAQAYQ	VAGLEKRAK	AGKRLAVHVL	VEPRVTNP-	-	-MDVQP	EDQGQRNSRF	YAK1WKG	-NFVRA	GNYT
ScOYE2	-ETGIVAQAYQ	VAGLEKRAK	AGKRLAVHVL	VEPRVTNP-	-	-EDBEE-NLAP	AARLMDG-	-PLTTEG	GEYGGNSDNP	VS1WKG
ScOYE3	-EPG11AQSY	VAGLEKRAK	AGKRLAVHVL	VEPRVTNP-	-	-	-	-	-	-
A36990	EE---IHSY	ILOQOORAD	NGOOLAYSLV	IEPVRITG-	-	-	-	-	-	-
	501	511	521	531	541	551	561	571	581	591
	-	-	-	-	-	-	-	-	-	-
SEQ 3	-NGKQ-	-AN QILEEQD-	-	-	-IDVALVG	RGFQKDPGLV	WTFQHQHLGV-	-	-	-
SEQ 6	-SAHILANS	LLKDQ	-	-	-LDLVLVG	RGFQKNPGLV	WAADELENV-	-	-EISMAN	QIRQGFTRRG
SEQ 8	ADEATAAEAM	LSGPEPK-	-	-	-ADAILIA	QFPLREPEWV	FSTARLKGV-	-	-EISMAN	QIRQGFTRRG
SEQ 10	-NGKQ-	-AN KILEEAG	-	-	-LDVALVG	RGFQKDPGLV	WTFQHQHLGV-	-	-PVTVPV	QFGRAI
SEQ 12	-KDPFLKL	KYLKEEGT	-	-	-FDLALIG	RGFPLRNPGLV	WEFADKLGV-	-	-EIANAS	QIRQGFTRRG
SEQ 14	-RDFKFLD	EPIANGD-	-	-	-FDIALIG	RGFKLNRNGL	SR1ADQLOA-	-	-RJLHOL	OLGWGFWPNK
SEQ 16	B-DGRVTTI	ERNGAKTR-	-	-	-ADMVLVA	RFQFLPEPFV	LTVADELGV-	-	-QFTRAP	QYKLALS
SEQ 19	-TRQME	AALESDD-	-	-	-COMIGIG	RFPAIINPSL	ANL1NPEV-	-	-DVKAJV	QYLRQPLSSR
SEQ 22	-TADI-	AR DWBDEQGAEK	VAEAKTHDT	IEVSESHGG	KTAKADLVLIA	RFQFLREPEV	LTAAHNLGV-	-	-PDADAV	LPDKGKRAPE
SEQ 24	-DGLFTTAN	E1LESQK-	-	-	-ADTVFVA	RFPLRNPNSL	LDSANQNLGE	-	-NQWMPV	QYHRAVMRKG
SEQ 27	-	-	-	-	-	-	-	-	-	-
SEQ 30	-TGHL-	-AE EVIQLSG-	-	-	-IDIVRAG	RWFQONPGLV	RAFANEGLV-	-	-NQAVMPV	QYDVAVKHGR
SEQ 33	-	-	-	-	-	-	-	-	-	-
SEQ 35	-	-	-	-	-	-	-	-	-	-
SEQ 38	-	-	-	-	-	-	-	-	-	-
SEQ 40	-	-	-	-	-	-	-	-	-	-
SEQ 42	-	-	-	-	-	-	-	-	-	-
SEQ 44	-VGAM-VDA	LOGVDG-	-	-	-IGIG	RAAGSEPDIA	KD11IAGKVSS	IIKYAMGEDE	FVLQLTACSA	QIRLMKGBE
SEQ 83	-IGTL-	-AE EIIAGG	-	-	-ED	DTPFLDLVAG	RLFQKNTGLV	WSSWADDLNT-	-S1QIAH	QIAQGFCGEE
SEQ 85	-VGMM-	EG SYDPSNG-	-	-	-	-QDROSIG	KLAEQSIQCS	ECDAVILAR-	-	-
Bacteria	-	-	-	-	-	-	-	-	-	-
T44612	-POLAE-	-AALOANO-	-	-	-LDLVSIG	RAHLADPHWA	YFAAAEKLGV-	-	-EKASWT	LPAPYAHWLE
NP_625402	-EPG-	-QAE KILANGE-	-	-	-ADAVLIG	RELLRNPNSA	QHARELGV-	-	-DARMPD	QYWGGM
NP_295913	-TGA-	-QAE AIIQAGD-	-	-	-ADLIALG	RPFRLRNPNSA	QHARELGLC-	-	-RPVSD	QYRAQGM-
AF320254	-AD-	-HAN SIIAAGR-	-	-	-ADLCIAA	RPHLADPAWT	LHEAAKIGF-	-	-GEVAWP	KYRSARGGY
OYE family	-	-	-	-	-	-	-	-	-	-
Af4875	-AASAEKFTQ	MAAATY-	-	-	-NVAIAF	RFYF1STPDLP	RFVFMAGIOL-	-	-QKYDVA	SYF5TSLREG
Af4961	-AGWDNSSN	GVLEBGR-	-	-	-YDALLYG	RFYF1STPDLV	ERLKGICPFF-	-	-TPYDVS	RFYGPFLSREG
Ca2460	-YDAPEFKTL	IHDLLND-	-	-	-RTIVGFA	RFYF1STPDLV	ERLKGICPFF-	-	-NHYDVR	RFYKQYNNY-G
Nc4452	-PETAK-	HLV DREPFKEK-	-	-	-DVAATPG	RFYF1STPDLV	ERLKGICPFF-	-	-NPYDVR	TPYKAKSPD
ScOYE1	-LHP-	-EVV REEVDFK-	-	-	-RTLICYG	RFYF1STPDLV	DRLEKGICPFF-	-	-NKYDVR	TPYKMSAE-H
ScOYE2	-LHP-	-EVV REEVDFP-	-	-	-RTLICYG	RFYF1STPDLV	DRLEKGICPFF-	-	-NKYDVR	TPYKMSAE-G
ScOYE3	-LHP-	-EVV REQVDFP-	-	-	-RTLICYG	RFYF1STPDLV	DRLEKGICPFF-	-	-NKYDVR	TPYKMSAE-G
A36990	-YDAPEFKTL	INDLND-	-	-	-RSI1GFS	RFYF1STPDLV	ERLKGICPFF-	-	-NYYNRS	TPYKQYNNY-G

	601	611	621	631
SEQ 3	GTPYIDPSVY	KQSIFDV-		
SEQ 6	AGPYLRKKLE	KI-----		
SEQ 8				
SEQ 10	GTPYIDPKAY	KESIPE---		
SEQ 12	QQIVDILERT	SKLEVN-----		
SEQ 14				
SEQ 16	PKKLTTVP-			
SEQ 19	WIVEKLGMKS	IVGAGVEVITW	YVSELKKLAK	F-----
SEQ 22	ARI-----			
SEQ 24	--KLR-----			
SEQ 27				
SEQ 30				
SEQ 33	KKVNKSSL-			
SEQ 35				
SEQ 38				
SEQ 40				
SEQ 42				
SEQ 44	PPFDISNADEV	ARVTQLMAGC	KV-----	
SEQ 83	KKNAPKLVL-			
SEQ 85	HRVHVAKK-			
Bacteria				
T44612	RYR-----			
NP_625402				
NP_295913				
AF320254	ETNLQRRAAA	VAGK-----		
OYE family				
Af4875	YIDYPPSAEY	MALAHNPPV-		
Af4961	KCYVDPYPAT	ASS-----		
Ca2460				
Nc4452	YIDQPSKEP	VIGKPLV-----		
ScOYE1	YIDYPTYEAA	LKLGWDKK-----		
ScOYE2	YIDYPTYEAA	LKLGWDKN-----		
ScOYE3	YTDYPTYEAA	VDLGWNKN-----		
A36990	YNSYDESEKQ	VIGKPLA-----		

Figure 1. A multiple alignment of the 2031 OR amino acid sequence from *A. fumigatus* (SEQ ID No3) along with related 2031 ORs from other fungi and bacteria (see Example 4) and OYES. Regions 1-11, marked with * or #, refer to amino acids conserved between ORs but not OYES.

Fungal 2031 ORs are given by the following SEQ ID No.: *A. fumigatus*, SEQ ID Nos. 3, 6 and 8; *A. nidulans*, SEQ ID No. 10; *C. albicans* SEQ ID Nos. 12 and 14; *N. crassa*, SEQ ID Nos. 16 and 19; *M. grisea* SEQ ID Nos. 22 and 44; *S. pombe* SEQ ID No. 24 (NP_595868); *C. trifolii* SEQ ID No. 27; *F. sporotrichioides* SEQ ID Nos. 30, 33 and 35; *F. graminearum* SEQ ID Nos. 38 and 83; *M. graminicola* SEQ ID Nos. 40 and 42; *U. maydis* SEQ ID No 85.

Bacterial ORs resembling 2031 are:

T44612 (*Pseudomonas putida*), SEQ ID No. 86; NP_625402 (*Streptomyces coelicolor*), SEQ ID No. 87; NP_295913 (*Deinococcus radiodurans*), SEQ ID No. 88; AF320254 (*Azoarcus evansii*, SEQ ID No. 89).

Fungal ORs similar to the Old Yellow Enzyme family (originally identified in *S. cerevisiae*):

A. fumigatus, Af4875 and Af4961, SEQ ID Nos. 90 and 91 respectively; *C. albicans*, Ca2460 and A36990, SEQ ID Nos. 92 and 93 respectively; *N. crassa*, Nc4452, SEQ ID No. 94; *S. cerevisiae*, OYE1, OYE2 and OYE3, SEQ ID Nos. 95-97 respectively.

Details of the sequence searches that identified the ORs other than SEQ ID No. 3, and methods for the construction of multiple alignments are given in Example 4 hereinafter.

	1	11	21	31	41	51	61	71	81	91
SEQ 1	GTTCGACGTC	ATPGCCACGT	TTCGACCCAA	GGGCAGACGC	CATGTCGCGG	AGCGATCGCC	GCGATATGCC	TCGAATTGTC	GCCATTGGC	ATCCAGTTTC
SEQ 2	-	-	-	-	-	-	-	-	-	-
SEQ 4	-	-	-	-	-	-	-	-	-	-
SEQ 5	-	-	-	-	-	-	-	-	-	-
SEQ 7	-	-	-	-	-	-	-	-	-	-
SEQ 9	-	-	-	-	-	-	-	-	-	-
SEQ 11	-	-	-	-	-	-	-	-	-	-
SEQ 13	-	-	-	-	-	-	-	-	-	-
SEQ 15	-	-	-	-	-	-	-	-	-	-
SEQ 17	-	-	-	-	-	-	-	-	-	-
SEQ 18	-	-	-	-	-	-	-	-	-	-
SEQ 20	-	-	-	-	-	-	-	-	-	-
SEQ 21	-	-	-	-	-	-	-	-	-	-
SEQ 23	-	-	-	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-
SEQ 28	-	-	-	-	-	-	-	-	-	-
SEQ 29	-	-	-	-	-	-	-	-	-	-
SEQ 32	-	-	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-
SEQ 36	-	-	-	-	-	-	-	-	-	-
SEQ 37	-	-	-	-	-	-	-	-	-	-
SEQ 39	-	-	-	-	-	-	-	-	-	-
SEQ 41	-	-	-	-	-	-	-	-	-	-
SEQ 43	-	-	-	-	-	-	-	-	-	-
SEQ 82	-	-	-	-	-	-	-	-	-	-
SEQ 84	-	-	-	-	-	-	-	-	-	-
	101	111	121	131	141	151	161	171	181	191
SEQ 1	CAGTGCCCTT	CCCCGAATGA	CTGTCCTCAC	TATTGGCAA	GATTTGAAAT	CAAGCCTGAA	GAAGCGGAGC	AATTCTTGGG	AGTCGTATGT	TCTACTGATT
SEQ 2	-	-	-	-	-	-	-	-	-	-
SEQ 4	-	-	-	-	-	-	-	-	-	-
SEQ 5	-	-	-	-	-	-	-	-	-	-
SEQ 7	-	-	-	-	-	-	-	-	-	-
SEQ 9	-	-	-	-	-	-	-	-	-	-
SEQ 11	-	-	-	-	-	-	-	-	-	-
SEQ 13	-	-	-	-	-	-	-	-	-	-
SEQ 15	-	-	-	-	-	-	-	-	-	-
SEQ 17	-	-	-	-	-	-	-	-	-	-
SEQ 18	-	-	-	-	-	-	-	-	-	-
SEQ 20	-	-	-	-	-	-	-	-	-	-
SEQ 21	-	-	-	-	-	-	-	-	-	-
SEQ 23	-	-	-	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-
SEQ 28	-	-	-	-	-	-	-	-	-	-
SEQ 29	-	-	-	-	-	-	-	-	-	-
SEQ 32	-	-	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-
SEQ 36	-	-	-	-	-	-	-	-	-	-
SEQ 37	-	-	-	-	-	-	-	-	-	-
SEQ 39	-	-	-	-	-	-	-	-	-	-
SEQ 41	-	-	-	-	-	-	-	-	-	-
SEQ 43	-	-	-	-	-	-	-	-	-	-
SEQ 82	-	-	-	-	-	-	-	-	-	-
SEQ 84	-	-	-	-	-	-	-	-	-	-
	201	211	221	231	241	251	261	271	281	291
SEQ 1	TCTGTGCTG	GGCCAGACGG	GTATATAAT	AAAGATCACC	GCACCGAGGA	GTTTCTTAC	AACCCATCAA	TAACCCATCA	CAATCTCTA	CAACAAAAAT
SEQ 2	TCTGTGCTG	GGCCAGACGG	GTATATAAT	AAAGATCACC	GCACCGAGGA	GTTTCTTAC	AACCCATCAA	TAACCCATCA	CAATCTCTA	CAACAAAAAT
SEQ 4	-	-	-	-	-	-	-	-	-	-
SEQ 5	-	-	-	-	-	-	-	-	-	-
SEQ 7	-	-	-	-	-	-	-	-	-	-
SEQ 9	-	-	-	-	-	-	-	-	-	-
SEQ 11	-	-	-	-	-	-	-	-	-	-
SEQ 13	-	-	-	-	-	-	-	-	-	-
SEQ 15	-	-	-	-	-	-	-	-	-	-
SEQ 17	-	-	-	-	-	-	-	-	-	-
SEQ 18	-	-	-	-	-	-	-	-	-	-
SEQ 20	-	-	-	-	-	-	-	-	-	-
SEQ 21	-	-	-	-	-	-	-	-	-	-
SEQ 23	-	-	-	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-
SEQ 28	-	-	-	-	-	-	-	-	-	-
SEQ 29	-	-	-	-	-	-	-	-	-	-
SEQ 32	-	-	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-
SEQ 36	-	-	-	-	-	-	-	-	-	-
SEQ 37	-	-	-	-	-	-	-	-	-	-
SEQ 39	-	-	-	-	-	-	-	-	-	-
SEQ 41	-	-	-	-	-	-	-	-	-	-
SEQ 43	-	-	-	-	-	-	-	-	-	-
SEQ 82	-	-	-	-	-	-	-	-	-	-
SEQ 84	-	-	-	-	-	-	-	-	-	-

	301	311	321	331	341	351	361	371	381	391		
SEQ 1	GACTGTGCC	GATATCGACG	TTCTCTTGC	CGAGGGCATC	CCCTACTTCA	CTCCGGCCCA	GAACCCCTCT	GCCGGTACCG	CAGCTAACCC	CCAGACCAAT	-----	
SEQ 2	GACTGTGCC	GATATCGACG	TTCTCTTGC	CGAGGGCATC	CCCTACTTCA	CTCCGGCCCA	GAACCCCTCT	GCCGGTACCG	CAGCTAACCC	CCAGACCAAT	-----	
SEQ 4	TGTTGTGCC	GACATCGAGA	ACAAACCCGC	GCCGGGTATC	TGTTACTTTA	CTCCGGCCCA	AGAGCCGCCT	GCTGGCACCG	CTGCTAATCC	TCAGTCTGAT	-----	
SEQ 5	TGTTGTGCC	GACATCGAGA	ACAAACCCGC	GCCGGGTATC	TGTTACTTTA	CTCCGGCCCA	AGAGCCGCCT	GCTGGCACCG	CTGCTAATCC	TCAGTCTGAT	-----	
SEQ 7	CGCCCTCCG	TCCCCCGCG	TCACCAAGTC	CTCCCTCAC	CCCTACTACA	CTCCGGCCAA	CAATGGAGGC	GCCGGCTCG	ACCCGAGCA	CCCCAC-----	-----	
SEQ 9	GGCTCTCCCT	GACGTGAA	ACACCCCGCG	GCCCGGCATC	CCCTACTTTA	CACAGACAA	GAACCCCTCT	GCTGGACAG	CTGCAAACCC	GCAAACCCAG	-----	
SEQ 11	AGTAAAACCA	TCAGATGAAA	TCAAAGGTGC	TCCTGAGGTT	TCCTATTACA	CTCCAGAAC	GCTGTCTCG	GCTGGTACTT	TTTATCCCC	ATGCTG-----A	-----	
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 15	CACCCAGAAG	AAGACCTCCT	CCCCCGCGC	CCCGGGTGT	CCCTTCTACA	CCCCGGCCCA	GGTCCCCGCC	GCCGGCCTC	CCCTCCCC	CACCCCC-----	-----	
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	ATGGCTACTT	CCACTACTTC	CGACCTC-----	
SEQ 18	GGCAGAAAAG	AAGACTTGA	GCACACCCGC	CGCCGGGTG	CTTACTACA	CCCCAGCCCA	GGAGCGCCCG	GCAGGGACCC	CTTTCAGCGA	GCAGGACG-----	-----	
SEQ 20	GGCAGAAAAG	AAGACTTGA	GCACACCCGC	CGCCGGGTG	CTTACTACA	CCCCAGCCCA	GGAGCGCCCG	GCAGGGACCC	CTTTCAGCGA	GCAGGACG-----	-----	
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 23	-----	ATGAC	TATTGTTAAT	GAAGGAGCG	AAAATGTTG	TTAATTATCA	CTCTGCGAAA	AAATACCGC	TGGAGCGCG	ATAGGTGTAC	CGCAA-----	-----
SEQ 25	CAGCATGACG	GGCACCGCGA	ACAAAGCGCG	CCCCGGTATC	CCGGTTATG	CCCCGGCCCA	GGAGCCTCCC	GGGGAAACGG	CAGTCAGCG	CAGCACCG-----	-----	
SEQ 26	-----	ATGACG	GGCACCGCGA	ACAAAGCGCG	CCCCGGTATG	CCGGTTATCA	CCCCGGCCCA	GGAGCCTCCC	CAGTCAGCG	CAGCACCG-----	-----	
SEQ 28	GGCTTACGAG	ATAATCGACA	ACGTTGCGGC	TGAAGGGTT	CCATATTACA	CACCGCTCA	AGACCCGCCA	GCTGGTACCG	AGACAAGCGG	CTAACCG-----	-----	
SEQ 29	GGCTTACGAG	ATAATCGACA	ACGTTGCGGC	TGAAGGGTT	CCATATTACA	CACCGCTCA	AGACCCGCCA	GCTGGTACCG	AGACAAGCGG	CTAACCG-----	-----	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 34	CCATACAAA	ATCATCATCA	ATAAGGAGC	TCCGAATGTT	CTTTCATATA	CTCCAGTGA	AGATCACCAC	GCAGGAACGG	CTTACGATGT	TCAGCTGAA-----	-----	
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 82	AAACAGGAG	GTTGTTAGA	ATGTCCTG	CAAAGGAGTG	CAATACTTCA	ACCCCTGAGCA	ACTTCTGCA	CCAGGTCTG	GTATAAACGG	TCCCAAT-----	-----	
SEQ 84	ACCGCCTCTC	GTGCACTCGA	TCGATGACT	CAAGATCAGC	AACTTTGTC	CCACTCGAAG	TGGCCACCC	CCTCTGTG	GGTCCCCGGA	ATCCATCTG	-----	
-----	401	411	421	431	441	451	461	471	481	491	-----	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 1	GG-----CC	AGAAGATCCC	CAAGCTCTTC	ACGGCCCTGA	CCATCCGTGG	CGTCACCC-----	-----	-----	TTCCAGAAC	CGCCCTGGTG	-----	
SEQ 2	GG-----CC	AGAAGATCCC	CAAGCTCTTC	ACGGCCCTGA	CCATCCGTGG	CGTCACCC-----	-----	-----	TTCCAGAAC	CGCCCTGGT-----	-----	
SEQ 4	GG-----AT	CGGCACCTCC	CAAGCTCTTC	CGGGCCGTTT	CGGTGCGGGG	TCTGACCC-----	-----	-----	TTTCACAAAT	CGCATTTGGCG	-----	
SEQ 5	GG-----AT	CGGCACCTCC	CAAGCTCTTC	CGGGCCGTTT	CGGTGCGGGG	TCTGACCC-----	-----	-----	TTTCACAAAT	CGCATTTGGC-----	-----	
SEQ 7	-----	GACCCC	TAGCGCTCTTC	CGGGCCCTTAC	AAATCCCGAA	TGTGACCC-----	-----	-----	CTCAAGAAC	CGCATCATG-----	-----	
SEQ 9	GG-----CA	ATGCCGCTCCC	CAAGCTGTTAC	ACACCTCTGA	CGGTGCGGTGG	GGTGACCC-----	-----	-----	TTCCACAAAC	AGACTTGGC-----	-----	
SEQ 11	GA-----TG	AAAGTTGCTCC	CAAATTTT	CAACCTTTAA	AGATTGTTAA	GCTTGTCT-----	-----	-----	TTGCCAAAC	AGAATTTGG-----	-----	
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	AC ATTACCTAAT	AGAATTTGG-----	-----	
SEQ 15	-----	G GCGATGCTCC	TACTCTCTTC	ACCCCTCTCA	AGATCCGTGG	CTCGATC-----	-----	-----	CTCCAGAAC	CGCTTGGCC-----	-----	
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	AC CCTCCCCAAC	CGCCCTGTC-----	-----	
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	AC CCTCCCCAAC	CGCCCTGTC-----	-----	
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	AC CTCCTCAAAC	CGCTTGGC-----	-----	
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	CTCTCCAAAC	CGCTTGGC-----	-----	
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	CTTCAAAAC	AGAATTTGG-----	-----	
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	ATCAACAAAC	CGCATCTGG-----	-----	
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	ATCAACAAAC	CGCATCTGG-----	-----	
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	TTCCAAAC	CGCCCTCTC-----	-----	
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	TTCCAAAC	CGCCCTCTC-----	-----	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	CTTCACAAAC	CGCCCTGGC-----	-----	
SEQ 34	GG-----	AAAGCTTAATTC	TCTCTTAAATA	AAATAAGAAA	CCTGACT	-----	-----	-----	CTTCAAAAC	CGGATTTTT-----	-----	
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	TTCCAAAC	CGTCTCTT-----	-----	
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	TTCCAAAC	CGTCTCTT-----	-----	
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	CTCCAGAAC	CGTATTATG-----	-----	
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	GGGCCCAAC	CGGTTCTC-----	
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	ATGCCCAAC	CGTATCTGG-----	
SEQ 84	CCAGGGGTG	TCAAAAAAAC	GGCTTGTTC	CAAAGTGTGA	CATTGCCCTT	TGCTGACCCG	GAACAGCCG	GTAAAGATGAC	CTTCAAGAAC	CGCATCATT-----	-----	
-----	501	511	521	531	541	551	561	571	581	591	-----	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 1	TAAGTCGTT	TGCCCTTGCT	CATATCGACG	AAAGCTTAATC	CCCCGTACAG-----	-----	-----	-----	CTCGC	GGCCCTCTGC	-----	
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	CTCGC	GGCCCTCTGC	-----	
SEQ 4	TGAGTGCAGT	CCAGGAATT	ATGCTATCCA	TCCTATGGGA	GCCCTTGAT	TGGAACAGCC	GCTTACAGGG	AATGATAATG	AGTAGCTATC	GCCACTCTGC	-----	
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	CTATC	GCCACTCTGC	-----	
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	GTGTC	GCCCATGTC	-----	
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	CTCGC	GGCCCTCTGC	-----	
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	GTATC	TCCAAATGTTG	-----	
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	GTTC	ACCAAATGTC	-----	
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	GTTC	GGCCATGTC	-----	
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	AAAGC	CGCCATGGCC	-----	
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	AAAGC	CGCCATGGCC	-----	
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	GCCCATGTC	-----	
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	GCCCATGTC	-----	
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	GCCCATGTC	-----	
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	GCCCATGTC	-----	
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	GCCCATGTC	-----	
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	CTTGC	CCCTCTCTGC	-----	
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	CTTGC	CCCTCTCTGC	-----	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	CCCTCTCTGC	-----	
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	CCCTCTCTGC	-----	
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	CTTGC	CCCTCTCTGC	-----	
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	CTTGC	CCCTCTCTGC	-----	
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	TTGAG	GGGGCTCTGC	-----	
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	AACGC	GGCCATGTC	-----	
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	CCCCATGTC	-----	
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	CCCCATGTC	-----	
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	GTCTC	TCCCATGTC	-----	

	601	611	621	631	641	651	661	671	681	691	
SEQ 1	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 2	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 4	CAATACTCAG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 5	CAATACTCAG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 7	ATGTACTCT	CGGAGTCGGA	CCCGTCGTCT	CCCCACGTG	CGCCCTCA	AAAC	-----	-----	-----	-----	
SEQ 9	CAGTACTCCG	CA	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 11	CAATATTCTG	CT	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 13	ATGTATTCTAT	CG	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 15	ACCTACTCTG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 17	GAACAAATGG	GC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 18	GAACAAATGG	GC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 20	ACCTACTCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 21	ACCTACTCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 23	ATCTATTCTCG	CT	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 25	CAGTACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 26	CAGTACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 28	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 29	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 34	CAATATTCTG	CA	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 36	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 37	CAATACTCCG	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 39	CAGTACTCTG	CT	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 43	GAGGGCTCTG	CG	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 82	CAATACAGT	CC	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 84	CAGTACTCTG	CG	-----	-----	-----	-----	-----	-----	-----	-----	
701	711	721	731	741	751	761	771	781	791	-----	
SEQ 1	CCGGCCCTGAT	GCTGTATGAG	GGCAGCCGGC	TCCAGCCCGA	A-----GGCCG	ATCACCCCTC	AGGATGTCGG	TCTGTGGAAAG	GACTCC-----	-----CA	
SEQ 2	CCGGCCCTGAT	GCTGTATGAG	GGCAGCCGGC	TCCAGCCCGA	A-----GGCCG	ATCACCCCTC	AGGATGTCGG	TCTGTGGAAAG	GACTCC-----	-----CA	
SEQ 4	CAGGATTCTT	GATGGTCGAG	GAACACAGCG	TGAAACCGGA	A-----GGCAGG	ATCACCCCG	AGGACCTGGG	ACTATGAAA	GACTCG-----	-----CA	
SEQ 5	CAGGATTCTT	GATGGTCGAG	GAACACAGCG	TGAAACCGGA	A-----GGCAGG	ATCACCCCG	AGGACCTGGG	ACTATGAAA	GACTCG-----	-----CA	
SEQ 7	CAGGCTCTGT	CTTCATCGAA	CCGACCGGG	TGACCGGAA	C-----GGCCG	ATCTCCCCCA	AGGACTCGGG	CCTCTGGAG	GACGGCACCA	CCTCGGAAACA	
SEQ 9	CCGGCTCTCAT	GATGGATCGG	GAACACCTGG	TCTCACCTGA	A-----GGCAGA	ATCACCGGGC	AGGACCTGGG	TCTATGGAAAG	GACTCG-----	-----CA	
SEQ 11	CAGGTATCAC	CATGGTGAAG	GGCACCGGT	TTTCTCTGA	G-----GGTGA	TTATCACCTC	ATGATTAGG	AATCTGGAA	GATGAA-----	-----CA	
SEQ 13	CAGCATTAAAT	CATTTTATGAG	AGTATCTTG	TGTCGAAAAA	T-----TCGGA	TTATCCATTC	ATGATTAGG	TCTTGGAAAT	GATGAT-----	-----CA	
SEQ 15	TCCCCCTCAT	CATCTCTGAG	GGCAGCCGG	TCTCTCCCCA	C-----GGCCG	ATCACCCCG	AGTCTCTCTG	TCTCTGGAG	GACTCC-----	-----CA	
SEQ 17	ACTGGGGCTC	GATTTCTTCCC	GGCAACGCTC	AAGTCGACAA	GGCGCACAC	GGGACGGCCC	AGGACATCGAC	CCCCAACCC	CCCCGACACA	CGCCCGAGGA	
SEQ 18	ACTGGGGCTC	GATTTCTTCCC	GGCAACGCTC	AAGTCGACAA	GGCGCACAC	GGGACGGCCC	AGGACATCGAC	CCCCAACCC	CCCCGACACA	CGCCCGAGGA	
SEQ 20	CGGCCCTGAC	CATGGTCGAG	GGCACATCGC	TCACCGCCAA	C-----GGACG	ATCTCGCCCG	AGGACAGCGG	CCTGTGGAG	GACAGC-----	-----CA	
SEQ 21	CGGCCCTGAC	CATGGTCGAG	GGCACATCGC	TCACCGCCAA	C-----GGACG	ATCTCGCCCG	AGGACAGCGG	CCTGTGGAG	GACAGC-----	-----CA	
SEQ 23	CTGGGCTCTGT	AAATGGTAGAG	GGCAGCCGG	TTTCCACCGA	G-----GGACG	ATTCACCTC	ATGATTAGG	ATTATGGATG	GACTCG-----	-----CA	
SEQ 25	CGGCCCTGTC	CATGGTCGAG	GGCACCCGG	TGGAGCTCG	T-----GGCCG	ATCTCCCCCG	AGGATGTCGG	TCTGTGGAG	GACTCG-----	-----CA	
SEQ 26	CGGCCCTGTC	CATGGTCGAG	GGCACCCGG	TGGAGCTCG	T-----GGCCG	ATCTCCCCCG	AGGATGTCGG	TCTGTGGAG	GACTCG-----	-----CA	
SEQ 28	CGGGATTGTC	CATGGTCGAG	GGTACCGCTG	TACAAAACCA	C-----GGTCG	ATCACACCTC	AGGATGTTGG	TCTGTGGAG	GACGGC-----	-----CA	
SEQ 29	CGGGATTGTC	CATGGTCGAG	GGTACCGCTG	TACAAAACCA	C-----GGTCG	ATCACACCTC	AGGATGTTGG	TCTGTGGAG	GACGGC-----	-----CA	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 34	CGGGCTCTCAT	TGTCACAGAA	GTCAACCGAG	TTTACCCAGA	G-----GGACG	ATCAGTCCTG	AGGATGCAAG	CATCTACGAT	GATGGG-----	-----CA	
SEQ 36	CGGGACTGTC	CATGGTAGAG	GGCACCGCTG	TTCAAAACCA	C-----GGTCG	ATCACCGCTC	AGGACGTTGG	TCTCTGGAGA	GATGGA-----	-----CA	
SEQ 37	CGGGACTGTC	CATGGTAGAG	GGCACCGCTG	TTCAAAACCA	C-----GGTCG	ATCACCGCTC	AGGACGTTGG	TCTCTGGAGA	GATGGA-----	-----CA	
SEQ 39	CGGGAACCTAC	CTGGCTTGTAA	GGCACACGGG	TCAGCTCCAT	A-----GGTCG	ATCACCGCTC	GATGTC-----	-----CA			
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 43	GGGGCCAGAT	CCAGACCGGG	AACGTATGA	TGACCCCGA	GCACCTGGAG	GCCCCGGGCA	ACATGGTTGG	GCCGGCCGAC	GCCGAGCCCT	CGGGCGAGCG	
SEQ 82	CTGGCCTCAT	CATGTCTAGAA	GCTACCCGG	TTCAAGCAG	T-----GGGCGT	ATCACACTG	AGGATTTCTG	CATCTGGCTA	GACTCT-----	-----CA	
SEQ 84	TGGGAAACGT	CATGGTCGAA	GGATCTTGTG	TTGAGCCAGA	G-----GGGAGG	ATCACCGCTC	AGGACCTGGG	TATTTGGTCTG	GAACAG-----	-----CA	
801	811	821	831	841	851	861	871	881	891	-----6	
SEQ 1	GATCGCCCG	-----ATGCGCC	GGGTCTATCGA	CTTCCTGTC	AGGCCAGGGC	CAGAAGATCG	GCGTG-----	CAGCTT	GCCCCATGCCG	GCCGGAAGAC	
SEQ 2	GATCGCCCG	-----ATGCGCC	GGGTCTATCGA	CTTCCTGTC	AGGCCAGGGC	CAGAAGATCG	GCGTG-----	CAGCTT	GCCCCATGCCG	GCCGGAAGAC	
SEQ 4	GATTGAGCC	-----TTGAGCC	GGGTCTATCGA	CTTCCTGTC	AGTCAGAAC	CAGCTTATCG	GCGTG-----	CAGATC	GCACACCGAC	GTCGGAAGGC	
SEQ 5	GATTGAGCC	-----TTGAGCC	GGGTCTATCGA	CTTCCTGTC	AGTCAGAAC	CAGCTTATCG	GCGTG-----	CAGATC	GCACACCGAC	GTCGGAAGGC	
SEQ 7	ATTCTGGGG	-----CTGAAAGC	GGGTCTATCGA	CTTCCTGTC	GCACAGGGC	GCCAAGTCG	GGATC-----	CAGCTT	GCGCATGCCG	GCCGGAAGAC	
SEQ 9	GATTGAGCC	-----CTGAAAGC	GGGTCTATCGA	CTTCCTGTC	GCACAGGGC	GCCAAGTCG	GGATC-----	CAGAT	GCCCCACCCG	GCCGGAAGGC	
SEQ 11	AGCAGAAAGAA	-----TTGAAAC	CAATGTCGAA	TTACGGCTAT	TCTCAAAAG	CAATTAATTG	CCATC-----	CAATG	GGCCATATGTC	GTAGAAAAGC	
SEQ 13	AGCTTCAGCT	-----TTACGGA	AAATTTGTTG	TTTATTTCTAT	GATCAAGAC	GGAAATTGTTG	GTATA-----	CAATG	AATCACCGTC	GGCGAAAGAT	
SEQ 15	GATTTGGCC	-----CTGAAAGC	GGATCTATCGA	CTTCATCCAT	TCCACGGG	CAGAAGGGC	GGTATC-----	CAGCTT	GCCCCACCCG	GCCGGAAGGC	
SEQ 17	GACCGTCACG	GCCTTCACGG	CCTGGCCGGA	CGCCGCGCGC	CTGAATGGC	CAGTCCAAA	CGCCTGTGTTG	CGTGCAGATC	AACCACCTG	GTCGCCAGAG	
SEQ 18	GACCGTCACG	GCCTTCACGG	CCTGGCCGGA	CGCCGCGCGC	CTGAATGGC	CAGTCCAAA	CGCCTGTGTTG	CGTGCAGATC	AACCACCTG	GTCGCCAGAG	
SEQ 20	GATCTGGCTCT	-----CTGGCC	GCATCTGTC	CTACGGTCAC	AGGCCAGGGC	CAAAAGATCG	CCATC-----	CAACTG	GTCATGCC	GCCGGAAGGC	
SEQ 21	GATCTGGCTCT	-----CTGGCC	GCATCTGTC	CTACGGTCAC	AGGCCAGGGC	CAAAAGATCG	CCATC-----	CAACTG	GTCATGCC	GCCGGAAGGC	
SEQ 23	AATGAAGCCG	-----TTACGGA	GAATTTGTTG	ATTGCTCAT	TCGCAAAAT	CAAAAATGTTG	GGAT-----	CAATG	GCGCATCTG	GTAGAAAAGC	
SEQ 25	GATTTGGCC	-----CTGAAAGC	GGATCTATCGA	CTTCATCCAC	TCGCAAGAC	CAGGTGCGGG	CCATC-----	CAGCTC	GCCCCACCCG	GTCGCAAGGC	
SEQ 26	GATTTGGCC	-----CTGAAAGC	GGATCTATCGA	CTTCATCCAC	TCGCAAGAC	CAGGTGCGGG	CCATC-----	CAGCTC	GCCCCACCCG	GTCGCAAGGC	
SEQ 28	GATCTGGCTCT	-----CTGAAAGC	GCATCCAC	TTTCGGCCAC	AGTCAGACG	CAGAAATTCG	GTATC-----	CAGCTG	TGGCATGCC	GTCGCAAGGC	
SEQ 29	GATCTGGCTCT	-----CTGAAAGC	GCATCCAC	TTTCGGCCAC	AGTCAGACG	CAGAAATTCG	GTATC-----	CAGCTG	TGGCATGCC	GTCGCAAGGC	
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 34	GCTTGACCT	-----CTCCGGG	ATATTTGTTG	CTTGTACAC	AGCCAGGGC	GCCAAGATTCG	CTAT-----	CAGATA	GGTCATGTC	GGAGAAAAGC	
SEQ 36	AATCGACCC	-----TTGAGCC	GCATCTACT	TTTGTCCAC	AGCCAGGGC	CAGAAGATTCG	GTAT-----	TCAGCTC	TGGCACCCG	GTGCTAAGGC	
SEQ 37	AATCGACCC	-----TTGAGCC	GCATCTACT	TTTGTCCAC	AGCCAGGGC	CAGAAGATTCG	GTAT-----	TCAGCTC	TGGCACCCG	GTGCTAAGGC	
SEQ 39	GATCGACCT	-----TTGCCAA	GGTCTGTC	GA	TTTGTCCAC	TCCCAAGAC	CAGAAGATTC	TGATT-----	CAGTTG	GGCAGATCCG	GGCGAAAGGC
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
SEQ 43	CTTCGACATG	-----TTTCAACG	TCGCGCCCGC	CGCCAAAGAG	CACGGCAGC	CTC-ATCGTC	GCG-----	CAGGTC	GGACACCCCG	GTGCCAGAGC	
SEQ 82	TGTTGAGGGA	-----CTCGGAA	AGCACGTCGA	TTTGTCCAC	GCCAACAC	TCTCTTATCG	GTATC-----	CAGATT	GGCCATATGTC	GTGCGAAGGC	
SEQ 84	TCGGGATGCA	-----CACAAGG	GGCTGTC	GGTGTCAAG	TCCCTCACG	GATGGTCTGG	GTGTA-----	GGGCTG	CAACTGGCCG	ATGCGGAGA	

	901	911	921	931	941	951	961	971	981	991
SEQ 1	CACCAACCGTT	GCGCCCTGGA	TCTCA-			-TTCTCGGCC	ATCGCGACGG	AGAAGGTGG	CGGATGCCG	
SEQ 2	CACCAACCGTT	GCGCCCTGGA	TCTCA-			-TTCTCGGCC	ATCGCGACGG	AGAAGGTGG	CGGATGCCG	
SEQ 4	CAGCACCGTC	GCGCCATGGC	TCTCG-			-GCCAACGAT	ACCGCCTCCG	AGAAGATGGG	CGGCTGGCC	
SEQ 5	CAGCACCGTC	GCGCCATGGC	TCTCG-			-GCCAACGAT	ACCGCCTCCG	AGAAGATGGG	CGGCTGGCC	
SEQ 7	GAGTGCCTT	GCGCCCTGCG	TGGCG-		-GGCC	AGGGGGGCAA	GTGCACTCTG	AGGGGGGATG	AGAGCGTTGG	CGGGTGGCCC
SEQ 9	TTCGAACATC	GCCCCCTGGC	TCATG-			-AA	CAAGGGCATC	GTGCGACGG	AGAAGGTGG	TGGCTGGCC
SEQ 11	TTCTGGTCAG	CCCCATATTTC	TGAC-			-TTGGAACAA	TTTGAGATA	AATCTGTCAA	TGGGTTTGGCC	
SEQ 13	TGTTGAAGGG	GTACCATTTCC	AACAA-					-ATACACAA	TGGTTGGCAA	
SEQ 15	CTCCACCAAG	GCCCCCTGGC	ACTAC-		-CAGCGCGG	CAAGAGCGAG	CTTGCCTGGC	CCGAGCAGGG	TGGCTGGCC	
SEQ 17	TCCGATGGGC	GCGGGCACGC	GGGGA-		-CTGT	GGGAGAAGGC	TGCGCGGCG	CGTGGGTGTT	GGGAGAGGG	
SEQ 18	TCCGATGGGC	GCGGGCACGC	GGGGA-		-CTGT	GGGAGAAGGC	GGTGGGGCCC	TGCGCGTGC	CGTGGGTGTT	GGGAGAGGG
SEQ 20	CAGCACAAAG	GCCCCCTGGC	ACGACTCTT	CACCCCGACG	GGCGAGTATA	AGGGAGAGA	GGGCTTACAG	GTGCTGCGAC	CCGAGATATGG	CGGCTGGCC
SEQ 21	CAGCACAAAG	GCCCCCTGGC	ACGACTCTT	CACCCCGACG	GGCGAGTATA	AGGGAGAGA	GGGCTTACAG	GTGCTGCGAC	CCGAGATATGG	CGGCTGGCC
SEQ 23	TAGGCAACT	GTCCTCTTATC	GAGGA-		-GAGGTCG	CGGCAAGGGC	CTGGCTCAG	AGAGCGAGAA	CGGCTGGCC	
SEQ 25	TAGGCACT	GCACCGTGG	TCACC-		-GAGGTCG	CGGCAAGGGC	CTGGCTCAG	AGAGCGAGAA	CGGCTGGCC	
SEQ 26	TAGGCACT	GCACCGTGG	TCACC-		-GAGGTCG	CGGCAAGGGC	CTGGCTCAG	AGAGCGAGAA	CGGCTGGCC	
SEQ 28	CAGTGGCTA	TCTCCCTGGC	TAAGC-		-GTAATGCT	TCGCGGGCG	AAGAATGTTG	TGCTCTGGCA		
SEQ 29	CAGTGGCTA	TCTCCCTGGC	TAAGC-		-GTAATGCT	TCGCGGGCG	AAGAATGTTG	TGCTCTGGCA		
SEQ 32										
SEQ 34	GAGCACAGTC	GTACCGTGG	TGGAC-		-CGAAGAAC	ACTGCTTTTA				
SEQ 36	TAGTTGTGA	TCTCCCTGGG	TGAGC-		-ATCAACGCT	TTTGCCTGA	AGGAAGTCGG	TGGCTGGCA		
SEQ 37	TAGTTGTGA	TCTCCCTGGG	TGAGC-		-ATCAACGCT	TTTGCCTGA	AGGAAGTCGG	TGGCTGGCA		
SEQ 39	GAGCACTGT	GCACCATGGT	TAAGC-		-GGCCGGAT	TTTGTGTGTT	AGGACGTCAA	CGGATGGCC		
SEQ 41					-GACT	GGCGAGAAA	CGGCCGC	AGGAGGGGG	AGGATGGCC	
SEQ 43	CCGGGGCACG	GTCCAGGAGC	ACCCC-		-ATTAGCGC	CAGCGACGT	CAGCTTAAG	AGGAGATGG		
SEQ 82	CTCCCTGGT	GCTCTCTGGG	TAGAC-		-GGCGACCT	GGCGCTGAAA	AGGCCGCTGG	TGGATGGCC		
SEQ 84	GAAGGCGCTCG	GACTGGTCAC	CTTTC-		-TACC	GGCGGAAAAAA	GAAGCAAAG	TTTGTGACGC	AGGAGGAAGG	TGGCTGGCC
	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091
				-7-						
SEQ 1	GACCCCGCT	AAAGGGCCCG	GGGATATC-			-CCCTTGGG	GGGCCCTTCG	CCAAGCCCCA	GGCCATGACG	
SEQ 2	GAC-CGGCTC	AAAGGGCCCG	GGGATATC			-CCCTTGGG	GGGCCCTTCG	CCAAGCCCCA	GGCCATGACG	
SEQ 4	GGC-CGGCTC	AAAGGGCCCG	CAAATGTG-			-CCCTTCACC	TTAAAGAAC	CTGTGCGGAA	GGAGATGACCC	
SEQ 5	GCG-CGGCTC	AAAGGGCCCG	CAAATGTG-			-CCCTTCACC	TTAAAGAAC	CTGTGCGGAA	GGAGATGACCC	
SEQ 7	GCG-GATGT	GTGGGTGGT	GGGGCGGG-		-GAGGAGC	ATATCTTTAG	TCCCGAGGAG	GATGCGTATT	GGGTGCGGCG	GGGCGTGCAG
SEQ 9	GAT-GATGT	ATCCGGCCGT	CCACCCGTG-			-CCCTTCAC	GAGACTTTCC	CCACCCCGAA	GGCCATGACCC	
SEQ 11	GAC-AAAGCA	GTGGCTCTT	CTGCGATG-		-GCATTC-	-AGACAAAT	GTGAAATTCT	CTGTTCTTAA	TGAGTTGAC	
SEQ 13	GAA-CATGTC	GTGGGCGAT	CTACTGAG-			-CCATTAGT	GATTACACAA	ATACACACG	AGAATTGACT	
SEQ 15	GAG-AACGTC	TGGGGCCCCA	GGGCCATC-			-AG	CTACACGAG	GAGACCTTC	CCITCCCCAA	GGAGATGACCC
SEQ 17	TTT-GTGCCT	CGGTTGTTGT	CGAAAGTGT-				-CTTTCG	GCACGCCG	GGAGCTGACG	
SEQ 18	TTT-GTGCCT	CGGTTGTTGT	CGAAAGTGT-				-CGGTTCTCG	GAGGACTTTC	CGAACCCCCA	GGAGATGAC
SEQ 20	GAT-GACGTC	TGGGGCCCCA	GGGCCATC-				-CGGTTCTCG	GAGGACTTTC	CGAACCCCCA	GGAGATGAC
SEQ 21	GAT-GACGTC	TGGGGCCCCA	GGGCCATC-				-GC	ACAAGAAAAT	GCTGTAAC	GGCTTCAAC
SEQ 23	AAT-GATGTT	TATGGACCAA	ATGAAGAC-				-AGGTTGGAC	GAAAGACCG	CTAACCTTC	TAAGTTAACT
SEQ 25	GAC-GACGTT	GTGGCTCCC	GGGGATT-				-CCTTACACC	AAGGACTTTC	CCACACGGG	TGAGTTGACT
SEQ 26	GAC-GACGTT	GTGGCTCCC	GGGGATT-				-CCTTACACC	AAGGACTTTC	CCACACGGG	TGAGTTGACT
SEQ 28	GAC-AATATC	GTGGCTCCC	CGGCCATC-				-GC	ACAAGAAAAT	GCTGTAAC	GGCTTCAAC
SEQ 29	GAC-AATATC	GTGGCTCCC	CGGCCATC-				-GC	ACAAGAAAAT	GCTGTAAC	GGCTTCAAC
SEQ 32										
SEQ 34										
SEQ 36	GAC-AACATT	GTGGCTCTT	CTGCCATC-				-GC	ACAAGAAGT	GGCGTGAC	CTGTTCCCCA
SEQ 37	GAC-AACATT	GTGGCTCTT	CTGCCATC-				-GC	ACAAGAAGT	GGCGTGAC	CTGTTCCCCA
SEQ 39	CAG-GATGTC	TGGGGCCCCA	GTGCGATT-				-CCATGGAC	GAGAAGCACG	CTGTTCCCCA	GGAGATGTCG
SEQ 41	GAG-GATGTT	GTGGGTGGT	CGGGTGGGGG	GGACTTTAG	TGGGATGAGA	GGTCCCTGAG	CGACCTTGT	GGAGGCTTGT	ATGGCCCGAG	AGAGTTGTCG
SEQ 43							-TTTGG	TCAAAGTTG	GGCGTGCAC	GGCCGCTAC
SEQ 82	GAT-GACGTT	GTCCGACCTA	CGAACAGAG-				-CCTTGTGCT	CCTGGGTTAC	CTACCCCCCG	TGCTTAACT
SEQ 84	GAT-CGGTTC	GTGGCTCTT	CGGCCATC-				-GCATATGCC	CAAGGTTCAC	TTACCCCCCG	AGCTCTCAC
	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191
SEQ 1	CTGGATGA-G	ATCGAGCAGT	TCAAGAAGGA	CTGGGTGGG	GCCACGAAGC	GGCCCATCGC	CG--CCGT	GGGGACTTTG	TCGAGATTCA	CAATGCCAT
SEQ 2	CTGGATGA-G	ATCGAGCAGT	TCAAGAAGGA	CTGGGTGGG	GCCACGAAGC	GGCCCATCGC	CG--CCGT	GGGGACTTTG	TCGAGATTCA	CAATGCCAT
SEQ 4	AAGCAGGA-T	ATCGAGGATC	TGAAGACCCG	CTGGGTGGG	GCTGTCACAC	GGGCTTGTAA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CAATGCCAT
SEQ 5	AAGCAGGA-T	ATCGAGGATC	TGAAGACCCG	CTGGGTGGG	GCTGTCACAC	GGGCTTGTAA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CAATGCCAT
SEQ 7	ACGGCCGA-G	GTCCGTCAAG	TGGGTGGGGC	TGGTGGAG	AGGCGCCGGC	TAGCGGTGCA	GG--CTGG	GGGGACTTTG	TCGAGATTCA	TGGGGCCAT
SEQ 9	AAGGACGA-C	ATCGAGGATC	TGAAGACCCG	CTGGGTGGG	TGGTGGAG	AGGCGCCGGC	GGGGACTTTG	TCGAGATTCA	CAATGCCAC	
SEQ 11	AAAGATGA-	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	GCTGTCAGAA	GGCTGTGAG	AATCAGTGG	TTTGTGTCAG	TTGAGATTCA	TGGTGTCTAT
SEQ 13	TTAATGA-T	ATAAACAGTC	TGTTGAAGA	TTTGTGTTG	GCTGTCAGAA	GGCTGTGAG	AATCAGTGG	TTTGTGTCAG	TTGAGATTCA	TGGTGTCTAT
SEQ 15	GTGGATGA-G	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	GCTGTCAGAA	GGCTGTGAG	TTTGTGTCAG	TTGAGATTCA	TGGTGTCTAT	
SEQ 17	GTGGATGA-G	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	ACGGCGAGGA	TCACGCCGGA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAC
SEQ 18	GTGGATGA-G	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	ACGGCGAGGA	TCACGCCGGA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 20	GTGGATGA-G	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	GCTGTCAGAC	GGTGGTGGG	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 22	GTGGATGA-G	ATCAACAGTC	TGTTGAAGA	TTTGTGTTG	GCTGTCAGAC	GGTGGTGGG	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 23	GAAAGGGA-A	TATGATGAAAT	TAGTGGATAA	TTTGTGTTG	GCTGTCAGAC	GGTGGTGGG	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 25	ACCGAGGRR	TGAGGAGGTCT	GGGTGAAGAA	TTTGTGTTG	GCTGTCAGAC	GGTGGTGGG	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 26	ACCGAGGRR	TGAGGAGGTCT	GGGTGAAGAA	TTTGTGTTG	GCTGTCAGAC	GGTGGTGGG	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 28	AAGGAGGA-T	ATAGACCAAC	TCAAGGCGA	CTACGGGAA	GCGCAAAAC	GAGCCATCCA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 29	AAGGAGGA-T	ATAGACCAAC	TCAAGGCGA	CTACGGGAA	GCGCAAAAC	GAGCCATCCA	GG--CCGG	GGGGACTTTG	TCGAGATTCA	CGCCGCCAT
SEQ 32										
SEQ 34										
SEQ 36	AAGGAGGA-T	ATCGAGGAAC	TCAAGAATGA	CTTTCCTGGCT	GGAGCMAAAC	GAGCCAWCCG	CGC--TGGT	TTTGTGATGTC	TCGAGATTCA	TGCACTCAT
SEQ 37	AAGGAGGA-T	ATCGAGGAAC	TCAAGAATGA	CTTTCCTGGCT	GGAGCMAAAC	GAGCCAWCCG	CGC--TGGT	TTTGTGATGTC	TCGAGATTCA	TGCACTCAT
SEQ 39	TTGATGA-T	ATCGAGGCTT	TCAAGAAGGC	GTGGTGGAG	GGCGTCACAG	GGGCTTGTAA	GG--TGG	TTTGTGATGTC	TCGAGATTCA	CAATGTCAT
SEQ 41	GTCAAGGA-G	ATCAAGGAGA	TTGGTCAAGA	CTTGGCGACA	GGAGCAGGAA	GGGCTTGTAA	GG--TGG	TTTGTGATGTC	TCGAGATTCA	CAATGTCAT
SEQ 43	AAGGAGGA-T	ATTAAGGCGG	TGATGAGGG	TTTGTGTTCC	GGGTGTGTC	GGAGCGTTG	AG--CAGGA	TTTGTGATGTC	TCGAGATTCA	CGCCGCCAC
SEQ 82	CTTGAGAGA-G	ATTGGAACAGT	TGAAGGAGGA	CTTGTGTTCC	GGGTGTGTC	GGAGCGTTG	AG--CAGGA	TTTGTGATGTC	TCGAGATTCA	TGCTCTCAC
SEQ 84	ACCGAGGA-C	ATCAACAGTC	TCAAGACAA	ATTGCTTCAG	TCGGCACAGT	GGGCGTTTGA	AG--CTGGG	TATGACTACG	TCGAGATTCA	CGCCGCCAT

	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291	
SEQ 1	GGATACCTGC	TGTCGTCAATT	CCTCTCGCCG	GCCGCCAAC	-	-	-	-	-	-	-
SEQ 2	GGATACCTGC	TGTCGTCAATT	CCTCTCGCCG	GCCGCCAAC	-	-	-	-	-	-	-
SEQ 4	GGCTATCTTC	TGATGTCGTT	CCTCTCCCT	GGGGTCAAC	-	-	-	-	-	-	-
SEQ 5	GGCTATCTTC	TGATGTCGTT	CCTCTCCCT	GGGGTCAAC	-	-	-	-	-	-	-
SEQ 7	GGCTATCTCA	TCAACGAGTT	CCTGAGCCCG	GTCAGAAAT	-	-	-	-	-	-	-
SEQ 9	GGGTATCTTC	TCTCGTCTTT	CCTATACCGG	TCTTCAAC	-	-	-	-	-	-	-
SEQ 11	GGTTATTGAGA	TTAACATGAGTT	CTATAGCTCT	ATTTCAAC	-	-	-	-	-	-	-
SEQ 13	GGATGTTTAA	TACACCAATT	TTAACGAA	-	-	-	-	-	-	-	-
SEQ 15	GGCTACCTCA	TTTCCGAGTT	CTTGAAGCCCG	ATCTCCAA	-	-	-	-	-	-	-
SEQ 17	GGATACCTGT	TGGCGCAGTT	CTTGAAGCAAG	AAGACAAAC	-	-	-	-	-	-	-
SEQ 18	GGATACCTGT	TGGCGCAGTT	CTTGAAGCAAG	AAGACAAAC	-	-	-	-	-	-	-
SEQ 20	GGTATACCTGA	TCACCGAGTT	CTTGGCCCG	CTATCAACG	TAAGTGGAGA	TACTTTGTGT	GGGGGTGTGC	GCATACTCCC	TCGGGTGTGA	CTTCTTAA	-
SEQ 21	GGTATACCTGA	TCACCGAGTT	CTTGGCCCG	CTATCAAC	-	-	-	-	-	-	-
SEQ 23	GGTTATCTTA	TATCGTCAAC	AGTTAGTCCT	GCCACTAAT	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-	-
SEQ 28	GGATATCTAC	TGCACTCAATT	CTTGAAGCCG	GTAAGCAAT	-	-	-	-	-	-	-
SEQ 29	GGATATCTAC	TGCACTCAATT	CTTGAAGCCG	GTAAGCAAT	-	-	-	-	-	-	-
SEQ 32	-	-	-	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-	-
SEQ 36	GGATACKTGC	TTCACCACTT	CTTGAAGTCCA	GTCAGTAAC	-	-	-	-	-	-	-
SEQ 37	GGATACKTGC	TTCACCACTT	CTTGAAGTCCA	GTCAGTAAC	-	-	-	-	-	-	-
SEQ 39	GGATACCTCC	TCCACCGAATT	CATCTGCCTG	AGAGCAAC	-	-	-	-	-	-	-
SEQ 41	GGGTACCTCA	TCCACCGAATT	CCTCTCACCC	ATTACCAAC	-	-	-	-	-	-	-
SEQ 43	GGTATACCTGC	TGGCCCAATT	CCTGTGCGAA	AACACCAAC	-	-	-	-	-	-	-
SEQ 82	GGTATACCTGT	TTTCACGCTT	CCTGTGCGCC	GCCACCAAC	-	-	-	-	-	-	-
SEQ 84	GGATACCTGA	TGCACTCGTT	CCTCAGCCCG	TTGACCAAT	-	-	-	-	-	-	-
	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391	
SEQ 1	-	-	-	-	-	-	-	-	-	-	-
SEQ 2	-	-	-	-	-	-	-	-	-	-	-
SEQ 4	-	-	-	-	-	-	-	-	-	-	-
SEQ 5	-	-	-	-	-	-	-	-	-	-	-
SEQ 7	-	-	-	-	-	-	-	-	-	-	-
SEQ 9	-	-	-	-	-	-	-	-	-	-	-
SEQ 11	-	-	-	-	-	-	-	-	-	-	-
SEQ 13	-	-	-	-	-	-	-	-	-	-	-
SEQ 15	-	-	-	-	-	-	-	-	-	-	-
SEQ 17	-	-	-	-	-	-	-	-	-	-	-
SEQ 18	-	-	-	-	-	-	-	-	-	-	-
SEQ 20	CATTTTATTT	CCTGGCACGC	AGAACCGAAC	AGACAGAAT	-	-	-	-	-	-	-
SEQ 21	-	-	-	-	-	-	-	-	-	-	-
SEQ 23	-	-	-	-	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-	-
SEQ 28	-	-	-	-	-	-	-	-	-	-	-
SEQ 29	-	-	-	-	-	-	-	-	-	-	-
SEQ 32	-	-	-	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-	-
SEQ 36	-	-	-	-	-	-	-	-	-	-	-
SEQ 37	-	-	-	-	-	-	-	-	-	-	-
SEQ 39	-	-	-	-	-	-	-	-	-	-	-
SEQ 41	-	-	-	-	-	-	-	-	-	-	-
SEQ 43	-	-	-	-	-	-	-	-	-	-	-
SEQ 82	-	-	-	-	-	-	-	-	-	-	-
SEQ 84	-	-	-	-	-	-	-	-	-	-	-
	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491	
SEQ 1	GCCGTCGGCC	CTCATGTGCC	C-	-	-	-	-	-	-	-	-
SEQ 2	GCCGTCGGCC	CTCATGTGCC	C-	-	-	-	-	-	-	-	-
SEQ 4	AAATGCCCCA	AGGATATGCC	T-	-	-	-	-	-	-	-	-
SEQ 5	AAATGCCCCA	AGGATATGCC	T-	-	-	-	-	-	-	-	-
SEQ 7	GTGATTCCCG	AGGGGATGCC	C-	-	-	-	-	-	-	-	-
SEQ 9	GCCGTCGGCC	CCAAACGTTC	T-	-	-	-	-	-	-	-	-
SEQ 11	AGTATTCAC	ACGATGTTCC	A-	-	-	-	-	-	-	-	-
SEQ 13	AAGATAGAAA	CA-----CC	G-	-	-	-	-	-	-	-	-
SEQ 15	GTCATCCCCG	AGGACATGCC	C-	-	-	-	-	-	-	-	-
SEQ 17	CAGGTACTG	AGGGGGTGGG	TGAAGAGGG	GCGAAGAAGT	TTGTTGGTGGG	AATCAAGCTG	AACAGTGGCG	ATTGGCAGGG	GGGACGCGAT	GGA-----	-
SEQ 18	CAGGTACTG	AGGGGGTGGG	TGAAGAGGG	GCGAAGAAGT	TTGTTGGTGGG	AATCAAGCTG	AACAGTGGCG	ATTGGCAGGG	GGGACGCGAT	GGAAG-----	-
SEQ 20	GTGATTCCCG	AGGAGATGCC	A-----	-	-	-	-	-	-	-	-
SEQ 21	GTGATTCCCG	AGGAGATGCC	A-----	-	-	-	-	-	-	-	-
SEQ 23	GCAATTCCAG	ATAGATGCC	C-----	-	-	-	-	-	-	-	-
SEQ 25	-	-	-	-	-	-	-	-	-	-	-
SEQ 26	-	-	-	-	-	-	-	-	-	-	-
SEQ 28	-	-	-	-	-	-	-	-	-	-	-
SEQ 29	-	-	-	-	-	-	-	-	-	-	-
SEQ 32	GCCATCCCCG	AAACTACACC	T-----	-	-	-	-	-	-	-	-
SEQ 34	-	-	-	-	-	-	-	-	-	-	-
SEQ 36	-	-	-	-	-	-	-	-	-	-	-
SEQ 37	-	-	-	-	-	-	-	-	-	-	-
SEQ 39	CAAT-----	-	-	-	-	-	-	-	-	-	-
SEQ 41	GCGATGCCC	CCAGCATGCC	T-----	-	-	-	-	-	-	-	-
SEQ 43	CGGACGAGCA	AGAATTTCAT	C-----	-	-	-	-	-	-	-	-
SEQ 82	GTATGCGCTG	AGGACATGCC	C-----	-	-	-	-	-	-	-	-
SEQ 84	GAATCCCCCA	ACAAGGGT-----	-	-	-	-	-	-	-	-	-

	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591
SEQ 1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-CGGGAGTC	GGCGAGCTGG	GATAT-----GC	AGAGCTCGT	GGAGCTGTC	AAAGAGCTG	CCGAATGGGG	CATTGACCTG	GTGAGATGTC	GCTCCGCCG
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	ACGAGTTTCC	TGAAAGCTGG	ACAGTCGAGC	AGACTT-----G	TCAACTCGCG	CGTATCTTC	CCAAGCATGG	AGTAGACTT	GTGGACGTCA	GCTCAGGGGG
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
SEQ 1	TGTTCTCCG	CAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	TGTTCTCCG	CAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	CACTCATTCG	GAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	CACTCATTCG	GAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	GAACACAAAG	GAC-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	TGTCAACGCC	GCG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	TAACGATTAT	AGA-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	AAATGTGCG	CAT-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	CAACAAACAG	GAC-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	TTATGAGGAT	CCTCAGTAA	GTTTGGGT	TGTTTGAGG	ATGGGGCAAG	GGTTGTCTG	TGTTGACCAA	CAAAGGGGC	ACGGAACAAA	TGCTAACGCC
SEQ 18	TTATGAGGAT	CCTCAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	AAACTCGGTG	GCC-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	AAACTCGGTG	GCC-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	TAATCACAAAG	GAT-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	TATCCATCT	AAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	GAATCATCT	CAG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	CTATGAGAGT	TTC-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	CATCCACAAAG	ATG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	CCTGGTCCA	TTC-----	-----	-----	-----	-----	-----	-----	-----	-----
	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791
SEQ 1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	ATACAGATGG	CCAACCGTCC	CAAGCCCGA	AAAGTCGAAC	GCACCATGG	CCGGCAGGCC	TTCTTCCTCG	AGTTGCCAA	GATCATCCG	ACCAAG-----T
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
SEQ 1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	-----AAGCT	GCTGGTGTGCC	GGCGTGGGTG	CCATCACCC-	-----	-----	-----	-----	-----	-----AACG GCAAGCAGGC
SEQ 4	-----AAACT	CGCAGTGGCA	TCAGTGGGTG	TGATTTGCC-	-----	-----	-----	-----	-----	-----AACG GCAAGCAGGC
SEQ 5	-----AAACT	CGCAGTGGCA	TCAGTGGGTG	TGATTTGCC-	-----	-----	-----	-----	-----	-----AGCG CGCATTTGGC
SEQ 7	-----GCTGG	CGCGTGGACT	CTTGTGGGTG	CTGTAGCTCT	GATCACCGAT	TCGGAACAGG	CGAGGGGACT	AGTTCAAGGA	CGGGACGAGG	CGACTGCAGC
SEQ 9	-----AAGCT	CCTTGTGGCG	ACCGTGGGCA	CGATCACCG-	-----	-----	-----	-----	-----	-----AACG GTAAGCAGGC
SEQ 11	-----AAGCT	ATTGGTCAGT	TGCGTGGGTG	GGCTTGA-	-----	-----	-----	-----	-----	-----A AAGATCTCTGA
SEQ 13	-----CGATG	TTTGATGCCA	TGCACTGGAG	GATTAGAT	-----	-----	-----	-----	-----	-----C GAGACATATT
SEQ 15	-----GCAAGCAGCT	CCTCGTGGT	GGCGTGGGTG	TGGTCACC-	-----	-----TCG	GCTGAGATCG	CCAAGGAGAC	CGTCCAGGAG	AAGGAGGATG GCAGAGTCAC
SEQ 17	-----TCCCCAAGCT	TCCCTCTCATG	GTCAACCGGG	GCTTCCGC-	-----	-----ACTC	GTCAGGGCAT	-----	-----	-----ACTC GTCAGGGCAT
SEQ 18	-----TCCCCAAGCT	TCCCTCTCATG	GTCAACCGGG	GCTTCCGC-	-----	-----	-----	-----	-----	-----ACGG CTGACATTGC
SEQ 20	-----AGGTT	GCTCATAGC	GGCGTGGGCA	ACATCAAC-	-----	-----	-----	-----	-----	-----ACGG CTGACATTGC
SEQ 21	-----AGGTT	GCTCATAGC	GGCGTGGGCA	ACATCAAC-	-----	-----	-----	-----	-----	-----ACGG CTGACATTGC
SEQ 23	-----AT	ACTACTTGGC	GCTGTGGAA	TGATCAGG-	-----	-----	-----	-----	-----	-----GATG GTCTTACGGC
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----AGTGT	ACTTGTTC	GCAGTAGGTG	GAATCAAG-	-----	-----	-----	-----	-----	-----A CTGGACATCT
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----ATGTT	GGTCTACACC	ACCGGGGGCT	TCAAGACG-	-----	-----	-----	-----	-----	-----GTGGGGC CCATGGTCGA
SEQ 43	-----AAGAT	GTGATCAGC	ACTGTGGT	GCATCAAG-	-----	-----	-----	-----	-----	-----ATAG GTACCCCTGC
SEQ 84	-----ATCGAAC	CGACGGTCC	AAACGATGC	TGCTCGGGG-	-----	-----	-----	-----	-----	-----CCGTGG GAATGATGGA
	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991
SEQ 1	GAATCAG-----	ATTCTAG	AGGAGCAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	GAATCAG-----	ATTCTAG	AGGAGCAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	CAATTC-----	TTGTTGG	AGAAGGAC-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	CAATTC-----	TTGTTGG	AGAAGGAC-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	CGAGGCAAT-----	CTGTCGGGAC	CTGAAACCC-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	GAACAAG-----	CTGCTT	AGGAGGAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	ATTGCTCAAC	AAATATTAG	AAGAAGGA-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	TTAACTCGAT	GAGTTTATTG	CTAAATGT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	CATCCACGG-----	GAGAACCGCC	CCAAAGACT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	GGAGGCC-----	GCTTTGG	AATCCGAT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 18	GGAGGCC-----	GCTTTGG	AATCCGAT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	GCGCGATGTC	GTGGATGAGC	AGGGCGCCGA	GAAGGTTGGC	GAGGCCAAGC	AGACGCATGA	CACCATCGAG	GTCGTGAGCG	AATCACATGG	CGGCAAGACCC
SEQ 21	GCGCGATGTC	GTGGATGAGC	AGGGCGCCGA	GAAGGTTGGC	GAGGCCAAGC	AGACGCATGA	CACCATCGAG	GTCGTGAGCG	AATCACATGG	CGGCAAGACCC
SEQ 23	GAATGAAATC	CTGAAAGTG	AAAAAGCT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	TGCTGAA-----	GAGGTTT	TGCAAATCT-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	CGCGCTGCA	GGCGTGGATG	GG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	GGAGGAG-----	ATCATCG	CTGGAGGGAGA	GGACGATACCC	-----	-----	-----	-----	-----	-----
SEQ 84	AGGTTC-----	TAACGATT	CGCCCAAC-----	-----	-----	-----	-----	-----	-----	-----
	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091
SEQ 1	GATATCGACG-----	TTGCGCTGGT	TGGCCGTGGG	TTCCAGAAGG	ATCCCGTCT	GGCTTGGAGC	TTTGCTCAGC	ACCTCGGGGT	C-----	-----
SEQ 2	GATATCGACG-----	TTGCGCTGGT	TGGCCGTGGG	TTCCAGAAGG	ATCCCGTCT	GGCTTGGAGC	TTTGCTCAGC	ACCTCGGGGT	C-----	-----
SEQ 4	GGACTGGACG-----	TTGCTGGTGT	TGGCGCTGGC	TTCCAGAAGA	ACCCGGGCT	GGTGTGGCG	TGGGCCAGCG	AGCTGAATGT	A-----	-----
SEQ 5	GGACTGGACG-----	TTGCTGGTGT	TGGCGCTGGC	TTCCAGAAGA	ACCCGGGCT	GGTGTGGCG	TGGGCCAGCG	AGCTGAATGT	A-----	-----
SEQ 7	AAGGGATG-----	CCATTCTGAT	AGCCCGTCAG	TTCTCGCGC	AGCCAGAATG	GGTGTGTTCC	ACGGCAGAA	AGTTGGGGT	G-----	-----
SEQ 9	GGATGGATG-----	TTGCGCTGTG	GGGAGCTGGT	TTCCAGAAGG	ATCCCGTCT	GGCGTGGAGCT	TTCGCGCAG	ATCTTGATGT	T-----	-----
SEQ 11	ACATTGATC	TGCTCTTGT	CTGGAGGAGA	TTTTCAGAAG	ATCCCGTCT	GGTATGGAG	TTTGGCGATA	AACTTGGGT	T-----	-----
SEQ 13	GACTTGTATA	TGACTTGTGAT	AGGTAAGGA	TTTCTCAAA	ACACTGGATT	GATCAGCCGT	ATTGCTGAGC	AACTGCAAGC	A-----	-----
SEQ 15	CGTCCGATATA	TGCTCTTGT	CTGGAGGAG	TTCTGGAG	AGCCCGTGT	CGTCTCTACT	GTCGCCAGCG	AGTIGGGTGT	T-----	-----
SEQ 17	GATIGGCACA	TGATCGGTAT	CGGACCCCGG	GCCATCATCA	ACCCCTGGCT	TCCCGCAAC	TTGATCCTCA	ACCCGGAGGT	G-----	-----
SEQ 18	GATIGGCACA	TGATCGGTAT	CGGACCCCGG	GCCATCATCA	ACCCCTGGCT	TCCCGCAAC	TTGATCCTCA	ACCCGGAGGT	G-----	-----
SEQ 20	AAGGGATC	TGCTCTTGT	CTGGCGCG	TTCTCGCGC	AGCCCTGAGT	TGTTGCTGAGG	ACGGGCGATA	ACCTTGGGGT	C-----	-----
SEQ 21	AAGGGATC	TGCTCTTGT	CTGGCGCG	TTCTCGCGC	AGCCCTGAGT	TGTTGCTGAGG	ACGGGCGATA	ACCTTGGGGT	C-----	-----
SEQ 23	-----GATG	TTACTTTGT	CGCAAGGGAG	TTCTTAAGGA	ACCCGTCGTT	GGTGTAGAC	AGCGCGAAC	AGTTGGGTGA	A-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	GGTATCGACA	TTGTGAGG	TGGACGTTGG	TTCCAAACAGA	ATCCCGTCT	GGTTCGAGCT	TTTGCTAACG	AGCTTGGGGT	G-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----ATAGGCAT	CGGGCGCCGA	GGCGGTTGG	AGCCGGACCT	CGCCAAGGAC	ATCATCGGG	GCAAGGTGTC	CAGCATTATC	AAATACGCCA	-----
SEQ 82	CCCTTGGATC	TTGTGCTT	AGGGCGCTGT	TTCCAGAAGA	ACACTGAGT	TGTTTGGTCA	TGGGCTGAGC	ATCTGAAACAC	T-----	-----
SEQ 84	GGCCAAGAC	GCAGCCAGAT	TGCAAGGTG	GGCGAGCGAT	CGATTCAAG	CGGAGAGTGT	GATGCGTAC	TGTTGGCACG	T-----	-----GGATTGA

	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
SEQ 1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	TGGGGGAGGA	CGAGTTTGTG	CTGCAGTTGA	CTGCTTGCTC	GGCCAAATA	AGCTGTATGG	CCAAGGGCGA	GGACCCCTTT	GAC-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	TGTCCTACCC	AAGCTGGACC	GAGGATGCTA	GTGTAGCGCT	GATGGTACCC	AGGGCAGCTG	GCAACCCGCA	GTACCATCGC	GTTCACGTGG	CTAAGAAGGT
	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
SEQ 1	GTACAAGCAG	TCTATTTCG	ATGTATAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 2	GTACAAGCAG	TCTATTTCG	ATGTATAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	CGAGAGATA	TAA-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	CGAGAGATA	TAA-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	TTATAAGGAG	AGCATCTTTG	AGTAA-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	AACATCTAAA	TTAGAAGTAA	ATTTAG-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	A-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	GTCCATTGTT	GGTGCCTGGTG	TTGAGGTGGT	ACGTACCGTT	CCAACCCCAT	TTGCTTCATT	GTGTTCCCGA	GTATGTCATG	CTGACTTGGT	TCTTTCTAG
SEQ 18	GTCCATTGTT	GGTGCCTGGTG	TTGAGGTGGT	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	G-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	A-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	A-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391
SEQ 1	AGTATAGATA	GAGTTGAAGA	TGATACCTCA	TAGACGATCA	ATGGACCCCTT	GCATATTATT	TCTCGTCTCC	TGCGTATGTT	CAAGGTATTTC	ACAGTAGCTG
SEQ 2	AGTATAGATA	GAGTTGAAGA	TGATACCTCA	TAGACGATCA	ATGGACCCCTT	GCATATTATT	T-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	ACGTGGTATG	TGAGCGAGCT	CAAGAAGCTG	GCCAAGTTTT	AG-----	-----	-----	-----	-----	-----
SEQ 18	ACGTGGTATG	TGAGCGAGCT	CAAGAAGCTG	GCCAAGTTTT	AG-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	GAGGGCAAGG	TG-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491
SEQ 1	CGTCCTCTTA	AGTTTCTCCG	TCATTCGTTTC	TATTCTACTC	CAATCGCAAC	GCATGGCGAC	CACGGATCGA	GTCGAATTTC	TCCGTCGTTC	GTATCTGATC
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591
SEQ 1	ATATATAAAA	GCGGGGAATG	GCTTGACCCC	GCGCAGAAATG	TCGATCTCTT	CGCAAACCTCT	CGGTGTATAG	GACGCTCAGC	AACGATCAAG	G
SEQ 2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 13	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 15	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 17	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 18	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 20	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 21	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 23	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 25	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 26	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 28	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 29	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 32	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 34	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 36	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 37	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 39	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 41	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 43	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 82	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SEQ 84	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Figure 2. A multiple alignments of the 2031 OR nucleic acid sequence from *A. fumigatus* (SEQ 1,2) along with related 2031 ORs from other fungi and bacteria (see also Example 4). Regions 1-11, marked with * or #, refer to regions conserved at the amino acid level between Ors but not OYES.

Fungal 2031 ORs are given by SEQ ID No.: SEQ ID Nos. 1, 2, 4, 5, and 7, *A. fumigatus*; SEQ ID No. 9, *A. nidulans*; SEQ ID Nos. 11 and 13, *C. albicans*; SEQ ID Nos. 15, 17 and 18, *N. crassa*; SEQ ID Nos. 20, 21 and 43, *M. grisea*; SEQ ID No. 23 (NP_595868), *S. pombe*; SEQ ID Nos. 25 and 26, *C. trifolii*; SEQ ID Nos. 28, 29, 31, 32 and 34, *F. sporotrichioides*; SEQ ID Nos. 36, 37 and 82, *F. graminearum*; SEQ ID Nos. 39 and 41, *M. graminicola*; SEQ ID No. 84, *U. maydis*.

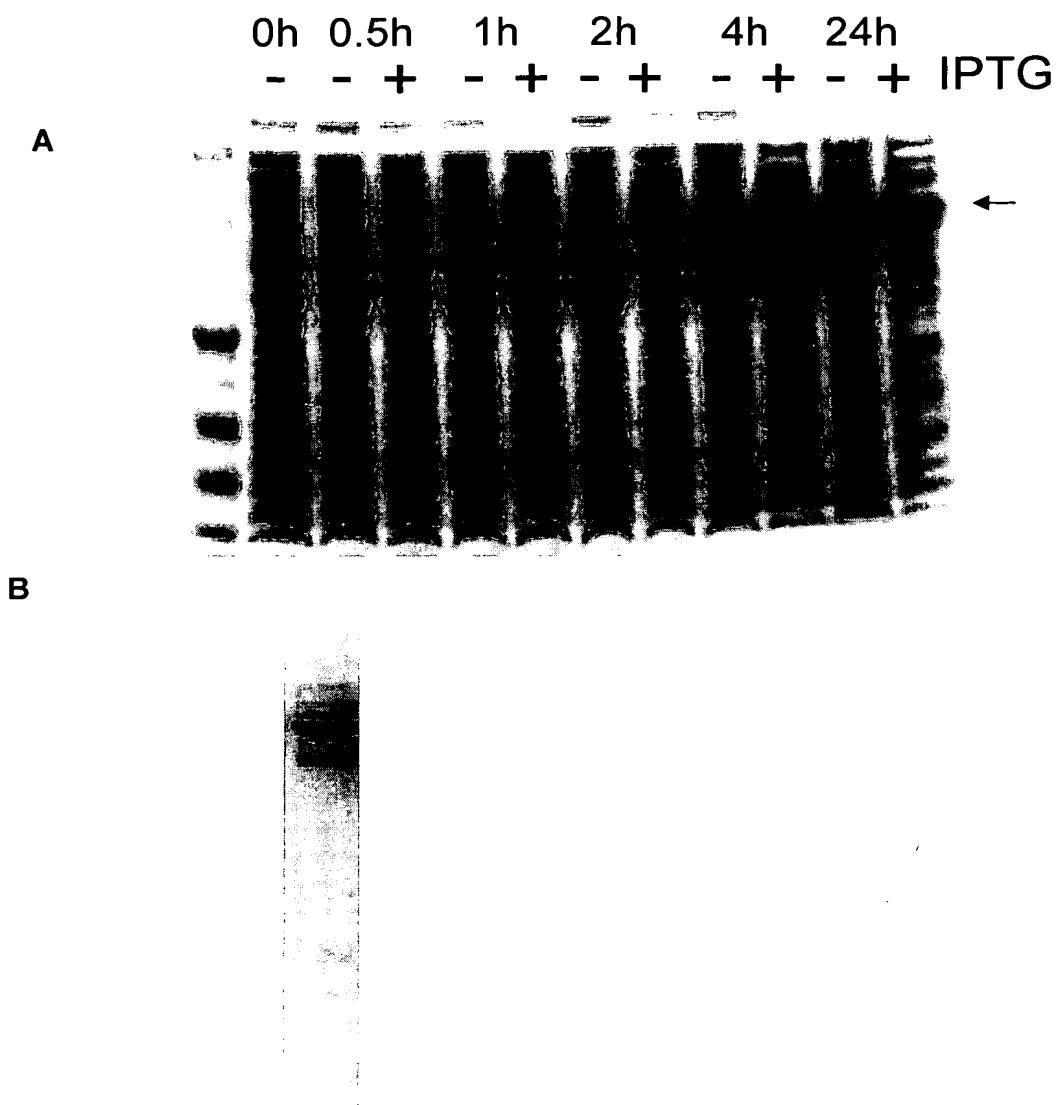


Figure 3. Recombinant 2031 OR. (A) Time course of recombinant 2031 OR induction over 24 hours after the addition of IPTG (samples without IPTG are also shown). The gel was stained with coomassie; A prominent band of the correct molecular weight (marked with an arrow) is seen. (B) Coomassie stained gel showing purified recombinant 2031.

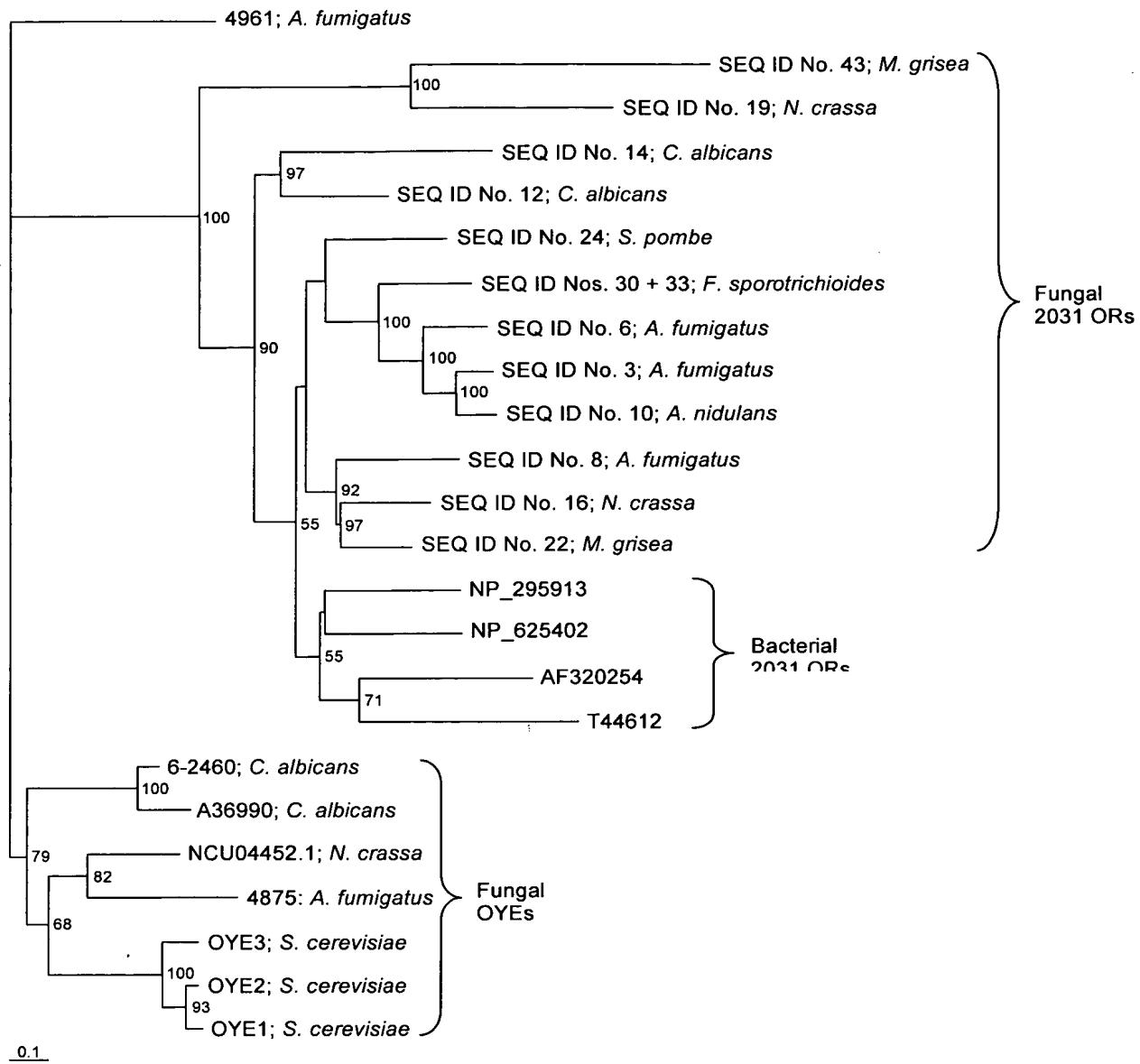


Figure 4. Phylogenetic tree showing relationships between *A. fumigatus* 2031 OR and similar proteins. This demonstrates a 2031 OR clade, which can be distinguished from the OYE proteins.

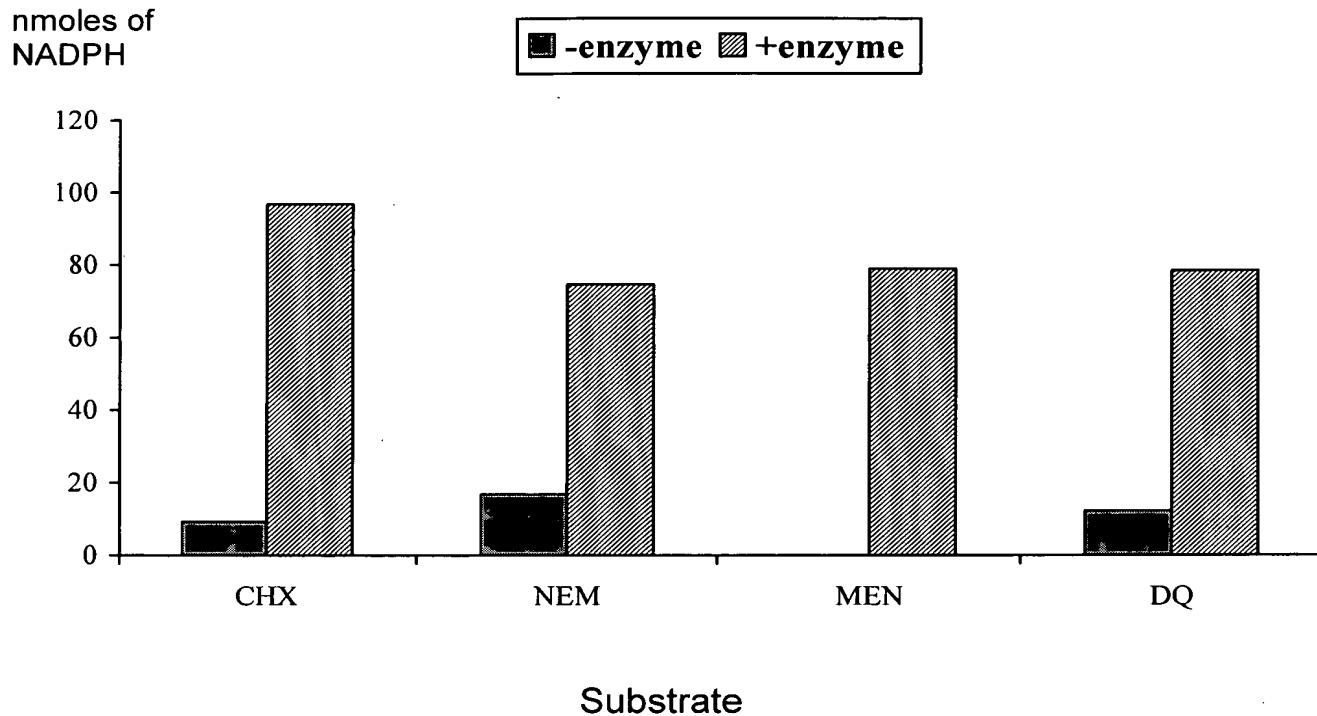


Figure 5: NADPH dehydrogenase activity of recombinant 2031 OR with cyclohexenone (CHX), N-ethylmaleimide (NEM), menadione (MEN) or duroquinone (DQ) as substrates. Final concentrations in the assay were as follows: 500 μ M substrate, 120 μ M NADPH, 1 μ g/200 μ L 2031 OR.

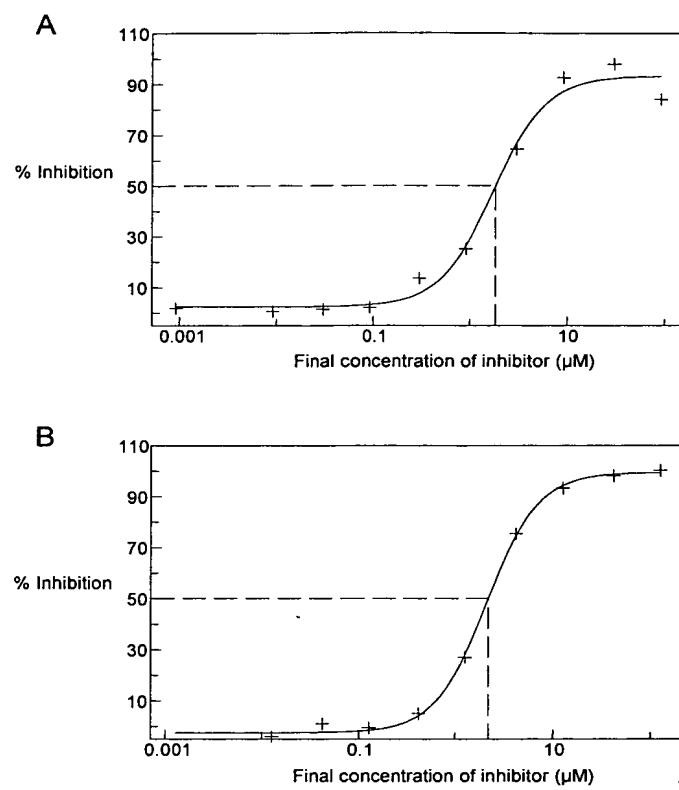


Figure 6: Inhibition of 2031 OR function by two inhibitors (shown in **A** and **B**) identified by high-throughput screening.